

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: June 28, 2002, 22:40:21 ; Search time 1381.16 Seconds
(without alignments)
22.376 Million cell updates/sec

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Title: US-09-709-170A-17
Perfect score: 18
Sequence: 1 tctccagcgtgcgccat 18

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched:      1736436 segs, 858457221 residues
Total number of hits satisfying chosen parameters
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Minimum	DB seq	length:	0
Maximum	DB seq	length:	75

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post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database :

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- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
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- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
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- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
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- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
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- 18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	16	AAO86595	Bcl-2 antisense ol
2	18	100.0	18	19	AAV52545	Unmethylated CpG d
3	18	100.0	18	19	AAV27719	Immunostimulatory
4	18	100.0	18	19	AAV28181	Antisense oligonuc
5	18	100.0	18	19	AAV19667	Human bcl-2 antisense
6	18	100.0	18	20	AAZ31944	CpG adjuvant oligo
7	18	100.0	18	20	AAZ41905	IL-2 secretion in
8	18	100.0	18	20	AAZ41948	IL-12 secretion in
9	18	100.0	18	20	AAV78803	HPV fusion protein

10	18	100.0	18	20	AAH8537
11	18	100.0	18	20	AAH33514
12	18	100.0	18	20	AAH23693
13	18	100.0	18	20	AAH27536
14	18	100.0	18	20	AAH18702
15	18	100.0	18	20	AAV99434
16	18	100.0	18	21	AAH64137
17	18	100.0	18	21	AAH60378
18	18	100.0	18	21	AAH65037
19	18	100.0	18	21	AAH90450
20	18	100.0	18	21	AAH91620
21	18	100.0	18	21	AAH39264
22	18	100.0	18	21	AAH14470
23	18	100.0	18	21	AAH38517
24	18	100.0	18	21	AAH99003
25	18	100.0	18	21	AAH60975
26	18	100.0	18	21	AAH279975
27	18	100.0	18	21	AAH28660
28	18	100.0	18	21	AAH247643
29	18	100.0	18	21	AAH247680
30	18	100.0	18	21	AAH247850
31	18	100.0	18	21	AAH247981
32	18	100.0	18	21	AAH248024
33	18	100.0	18	22	AAH50615
34	18	100.0	18	22	AAH20395
35	18	100.0	18	22	AAH98832
36	18	100.0	18	22	AAH98885
37	18	100.0	18	22	AAH98929
38	18	100.0	18	22	AAH98930
39	18	100.0	18	22	AAH98966
40	18	100.0	18	22	AAH60923
41	18	100.0	18	22	AAH59502
42	18	100.0	18	22	AAH27748
43	18	100.0	18	22	AAH92362
44	18	100.0	18	22	AAH19305
45	18	100.0	18	22	AAH19305

DR WPI: 1995-139394/18.
 XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Example 18: Page 44; 108pp; English.
 XX
 CC Reversal of chemoresistance of tumor cells by antisense-mediated
 CC reduction of bcl-2 expression was demonstrated using the
 CC oligonucleotide given in AA086659. This is antisense to the first
 CC 6 codons of the bcl-2 ORF.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 XX
 Query Match 100.0%; Score 18; DB 16; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tctccacagctgcgcacat 18
 Db 1 tctccacagctgcgcacat 18
 XX
 RESULT 2
 AAV52545
 ID AAV52545 standard; DNA; 18 BP.
 XX
 AC AAV52545;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Unmethylated Cpg dinucleotide 1758.
 XX
 KW Unmethylated Cpg dinucleotide; immune response; bacterial meningitis;
 KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KW pulmonary disorder; asthma; environmentally induced airway disease;
 KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KW inflammatory bowel disease; ss.
 XX
 OS Synthetic.
 XX
 PN WO9837919-A1.
 XX
 PD 03-SEP-1998.
 XX
 PR 25-FEB-1998; 98WO-US03678.
 XX
 PR 28-FEB-1997; 97US-0039405.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Krieg AM, Schwartz DA;
 XX
 DR WPI: 1998-480941/41.
 XX
 PT Use of nucleic acids containing an unmethylated Cpg - for treating a
 PT subject having or at risk of having an acute decrement in air flow
 PT or inhibiting an inflammatory response
 XX
 PS Example 4; Page 35; 65pp; English.
 XX
 CC This sequence represents an unmethylated Cpg dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing at least one
 CC unmethylated Cpg. The nucleic acid sequence containing at least one
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an
 CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with

CC Gram-positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide.
 XX
 SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 XX
 Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tctccacagctgcgcacat 18
 Db 1 tctccacagctgcgcacat 18
 XX
 RESULT 3
 AAV27719
 ID AAV27719 standard; DNA; 18 BP.
 XX
 AC AAV27719;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Immunostimulatory oligodeoxyribonucleotide of the invention.
 XX
 KW Immunostimulatory; oligodeoxyribonucleotide; ODN.
 KW unmethylated Cpg dinucleotide; activate; lymphocyte; immune response;
 KW Th2; Th1; cytokine; treatment; prevention; asthma; autoimmune disease;
 KW desensitisation therapy; artificial adjuvant; antibody generation; ss.
 XX
 OS Synthetic.
 XX
 PN WO9818810-A1.
 XX
 PD 07-MAY-1998.
 XX
 PR 30-OCT-1997; 97WO-US19791.
 XX
 PR 30-OCT-1996; 96US-0738652.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Kline JN, Krieg AM;
 XX
 DR WPI: 1998-272127/24.
 XX
 PT New immunostimulatory nucleic acid molecules - which contain at
 PT least one unmethylated Cpg dinucleotide, used for treating e.g.
 PT tumours, infections or autoimmune disease
 XX
 PS Disclosure; Page 49; 109pp; English.
 XX
 CC AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides
 CC (ODNs) of the invention. The ODNs contain at least one unmethylated Cpg
 CC dinucleotide, and have the formula:
 CC 5' N1X1G4X2N2 3', where at least one nucleotide separates consecutive
 CC Cpgs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N
 CC is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and
 CC OR 5' N1X12CGX3X4N 3', where at least one nucleotide separates
 CC consecutive Cpgs, X1 and X2 are selected from GPT, GPC, GPA, APT and APA,
 CC X3 and X4 are selected from TPT or CPT, N is any nucleotide and N1+N2 is
 CC 0-26 bases with the provision that N1 and N2 does not contain a CCG
 CC tetramer or more than one CCG or CCG trimer.
 CC The ODNs activate lymphocytes in a subject and redirect a subject's
 CC immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells
 CC and other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
 CC GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,
 CC autoimmune diseases, in desensitisation therapy, as an artificial
 CC adjuvant during antibody generation in a mammal such as a mouse or a

CC human.
 XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 4

AAV28181
 ID AAV28181 standard; DNA; 18 BP.

XX AAV28181;

AC 08-OCT-1998 (first entry)

XX Antisense oligonucleotide to bcl-2 mRNA.

DE Purification: oligonucleotide; matrix; affinity unit;

XX affinity purification; antisense; bcl-2; ss.

OS Synthetic.

XX WO9827425-A1.

PN 25-JUN-1998.

XX 18-DEC-1997; 97WO-US23284.

PF 19-DEC-1996; 96US-0769951.

PR (ISIS-) ISIS PHARM INC.

XX Chen D, Cole DL, Srivatsa GS;

PI WPI; 1998-362922/31.

DR Matrix for selective separation of oligo:nucleotide - useful for,

PT e.g. large scale purification of anti-sense agents from their

PT deletion derivatives formed during synthesis

XX Disclosure; Page 86; 183pp; English.

XX AAV28181-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridising portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 5

AAV19667
 ID AAV19667 standard; DNA; 18 BP.

XX AAV19667;

AC 12-JUN-1998 (first entry)

XX Human bcl-2 antisense oligonucleotide 13.

DE Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

XX cancer; ss.

OS Synthetic.

XX Homo sapiens.

XX US5734033-A.

XX 31-MAR-1998.

XX 24-MAR-1994; 94US-0288692.

XX 21-FEB-1992; 92US-0840716.

XX 22-DEC-1988; 88US-0288692.

XX 24-MAR-1994; 94US-0217082.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Read J;

XX WPI; 1998-229881/20.

XX Antisense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

XX Disclosure; Column 23; 21pp; English.

XX This antisense oligonucleotide is complementary to the translation
 CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
 CC oligonucleotides are phosphorothioate derivatives and can straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of
 CC a functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
 SQ

Query Match 100.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 ||||||||||||||||
 Db 1 tctccagcgtgcgcacat 18

RESULT 6

AAZ31944
 ID AAZ31944 standard; DNA; 18 BP.

XX AAZ31944;

XX 26-JAN-2000 (first entry)

XX Cpg adjuvant oligo 1002.

XX Cpg adjuvant; vaccine; polyoxyethylene ether; polyoxyethylene ester;

XX antigen; infection; allergy; cancer; therapy; ss.

XX Synthetic.

XX PN W09952549-A1.
 XX PD 21-OCT-1999.
 XX PF 29-MAR-1999; 99WO-EP02278.
 XX PR 09-APR-1998; 98GB-0007805.
 XX PR 25-SEP-1998; 98GB-0020956.
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX PI Friede M, Hermand P;
 XX DR WPI; 1999-620290/53.
 XX PT Vaccine to protect against infections, allergy and cancer -
 XX PS Example 9; Page 26; 52pp; English.
 CC This sequence represents a Cpg adjuvant that can be used in the vaccine
 CC composition of the invention. The vaccine comprises a polyoxyethylene
 CC ether or ester (I), not in the form of a vesicle, pharmaceutically
 CC acceptable excipient and an antigen (Ag) or antigenic composition. The
 CC vaccine can be used to treat or prevent infections (by bacteria, viruses
 CC or other parasites), allergy and cancer. (I), which are safe, easy to
 CC sterilize and simple to administer, are powerful vaccine adjuvants, able
 CC to induce a systemic immune response when administered (non-invasively)
 CC to the mucosa. The response is at least as good as that from conventional
 CC reactogenicity and are well tolerated.
 XX SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 20; Length 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 Db 1 tctccagcgtgcgcacat 18

RESULT 7
 AAZ41905
 ID AAZ41905 standard; DNA; 18 BP.
 XX AC AAZ41905;
 XX DT 24-JAN-2000 (first entry)
 XX DE IL-12 secretion inducing Cpg oligonucleotide 50.
 XX KW Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
 XX KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
 XX KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
 XX KW antigen presenting cell; infection; allergic disease.
 XX OS Synthetic.
 XX PN W09951259-A2.
 XX PD 14-OCT-1999.
 XX PF 02-APR-1999; 99WO-US07335.
 XX PR 03-APR-1998; 98US-0080729.
 XX PA (IOWA) UNIV IOWA RES FOUND.
 XX PI Krieg AM, Weiner G;
 XX

DR WPI; 1999-620169/53.
 XX XX Novel synergistic combinations of immunostimulatory oligonucleotides
 XX PT and immunopotentiating cytokines are useful for stimulating the immune
 XX PT system -
 XX PS Example 8; Page 80; 91pp; English.
 XX CC Sequences AAZ41856-241949 are phosphorothioate Cpg oligonucleotides
 XX CC which are used in the invention to induce Interleukin-12 (IL-12)
 XX CC secretion from human PBMC. The invention comprises stimulating an immune
 XX CC response in a subject comprising administering to a subject exposed to an
 XX CC antigen, an immunopotentiating cytokine and an immunostimulatory Cpg
 XX CC oligonucleotide to induce a synergistic antigen specific immune
 XX CC response. The methods are useful for treating cancer by stimulating an
 XX CC antigen specific immune response against a cancer antigen. The methods
 XX CC can also be used to treat neoplastic disorders in humans, including but
 XX CC not limited to: sarcoma, carcinoma, fibroma, lymphoma, melanoma,
 XX CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
 XX CC for treating infectious diseases, e.g. viral diseases such as HIV,
 XX CC bacterial diseases, and fungal diseases. The methods may also be used to
 XX CC treat allergic diseases, e.g. asthma. The methods and compositions may
 XX CC also be applied to treat cancer and tumors in non human subjects,
 XX CC e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
 XX CC be treated and include leukaemia, haemangioepithelioma and bovine ocular
 XX CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
 XX CC caused by the bacterium Corynebacterium pseudotuberculosis, and
 XX CC treated. Cpg oligonucleotides can be useful in activating B cells, NK
 XX CC cells, and antigen presenting cells, such as monocytes and macrophages.
 XX CC Cpg oligonucleotides enhance antibody dependent cellular cytotoxicity and
 XX CC can be used as an adjuvant in conjunction with tumour antigens to
 XX CC protect against a tumour challenge.

SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match
 Best Local Similarity 100.0%; Score 18; DB 20; Length 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tctccagcgtgcgcacat 18
 Db 1 tctccagcgtgcgcacat 18

RESULT 8
 AAZ41948
 ID AAZ41948 standard; DNA; 18 BP.
 XX AC AAZ41948;
 XX DT 24-JAN-2000 (first entry)
 XX DE IL-12 secretion inducing Cpg oligonucleotide 93.
 XX KW Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
 XX KW human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
 XX KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
 XX KW antigen presenting cell; infection; allergic disease.
 XX OS Synthetic.
 XX PN W09951259-A2.
 XX PD 14-OCT-1999.
 XX PF 02-APR-1999; 99WO-US07335.
 XX PR 03-APR-1998; 98US-0080729.
 XX PA (IOWA) UNIV IOWA RES FOUND.
 XX

PI Krieg AM, Weiner G;
XX
XX WPI: 1999-620169/53.
PT Novel synergistic combinations of immunostimulatory oligonucleotides
PT and immunopotentiating cytokines are useful for stimulating the immune
PT system -
XX
XX Example 8; Page 88; 91pp; English.
XX
XX Sequences AA241856-241949 are phosphorothioate Cpg oligonucleotides
CC which are used in the invention to induce interleukin-12 (IL-12)
CC secretion from human PBMC. The invention comprises stimulating an immune
CC response in a subject comprising administering to a subject exposed to an
CC antigen, an immunopotentiating cytokine and an immunostimulatory Cpg
CC oligonucleotide to induce a synergistic antigen specific immune
CC response. The methods are useful for treating cancer by stimulating an
CC antigen specific immune response against a cancer antigen. The methods
CC can also be used to treat neoplastic disorders in humans, including but
CC not limited to: sarcoma, carcinoma, fibroma, lymphoma, melanoma,
CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC for treating infectious diseases, e.g. viral diseases such as HIV,
CC bacterial diseases, and fungal diseases. The methods may also be used to
CC treat allergic diseases, e.g. asthma. The methods and compositions may
CC also be applied to treat cancer and tumours in non human subjects, e.g.
CC cats and dogs. Neoplasias affecting agricultural livestock may also
CC be treated and include leukaemia, haemangiosarcoma and bovine ocular
CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC caused by the bacterium *Corynebacterium pseudotuberculosis*, and
CC contagious lung tumour of sheep caused by *Jaagsiekte* may also be
CC treated. Cpg oligonucleotides can be useful in activating B cells, NK
CC cells, and antigen presenting cells, such as monocytes and macrophages.
CC Cpg oligonucleotides enhance antibody dependent cellular cytotoxicity and
CC can be used as an adjuvant in conjunction with tumour antigens to
CC protect against a tumour challenge.
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tctccagcgtgcgcacat 18
| | | | | | | | | | | | | | | | | |
Db 1 tctccagcgtgcgcacat 18

RESULT 9
AA278803 standard; DNA; 18 BP.
XX
XX AAX78803;
AC
XX 06-SEP-1999 (first entry)
DT
XX
XX HPV fusion protein Cpg oligonucleotide 2.
DE
XX
XX Fusion protein: E6 protein; E7 protein; immunomodulator; tumour;
KW immunological fusion partner; Cpg oligonucleotide; immune response;
KW HPV antigen; prevention; treatment; primer; ss.
XX
XX Synthetic.
OS Human papillomavirus.
XX
XX WO9933868-A2.
PN
XX
XX 08-JUL-1999.
PD
XX 18-DEC-1998; 98WO-EP08563.
PF
XX 24-DEC-1997; 97GB-0027262.
PR
XX

PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
PI
XX
XX WPI: 1999-405485/34.
DR
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV
PT
XX
XX Claim 11; Page 37; 62pp; English.
XX
XX AA278791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AA25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory Cpg
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used
CC for preventing or treating HPV induced tumours. This sequence represents
CC a Cpg oligonucleotide which is used in the method of the invention.
XX
XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tctccagcgtgcgcacat 18
| | | | | | | | | | | | | | | | | |
Db 1 tctccagcgtgcgcacat 18

RESULT 10
AA288537 standard; DNA; 18 BP.
XX
XX AAX88537;
AC
XX
XX 10-SEP-1999 (first entry)
DT
XX
XX Cytosine-guanosine dinucleotide motif oligonucleotide #4.
DE
XX
XX Cytosine-guanosine dinucleotide motif; Cpg; immunomodulation;
KW unmethylated; vaccine; immunostimulation; immune response;
KW T-independent type 1 antigen; T-independent type 2 antigen;
KW polysaccharide conjugate antigen; ss.
XX
XX
XX Synthetic.
OS
XX
XX WO9933488-A2.
PN
XX
XX 08-JUL-1999.
PD
XX
XX 18-DEC-1998; 98WO-EP08562.
PF
XX
XX 24-DEC-1997; 97GB-0027262.
PR
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX
XX Dalemans WLJ, Laferrere CAJ, Prieels J;
PI
XX
XX WPI: 1999-405369/34.
DR
XX
XX A vaccine composition for inducing an immune response to
PT T-independent type 1 or type 2 antigen or polysaccharide conjugate
PT antigen
PT
XX
XX Claim 6; Page 31; 35pp; English.
XX
XX The present invention describes a formulation (A) comprising a
CC cytosine-guanosine dinucleotide motif (Cpg) oligonucleotide and
CC T-independent type 1 or type 2 antigens or polysaccharide conjugate
CC antigen. The present sequence represent a specifically claimed Cpg

CC oligonucleotide. A vaccine composition comprising the formulation is
CC used for inducing an immune response to T-independent type 1 or type 2
CC antigen or polysaccharide conjugate antigen. The use of
CC immunostimulatory CpG oligonucleotide acts as an adjuvant to
CC pneumococcal polysaccharides.
XX
SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccagcgtgcgcacat 18
Db 1 tctccagcgtgcgcacat 18

RESULT 11

AAK33514
ID AAK33514 standard; DNA; 18 BP.

XX AAK33514;

DT 07-JUL-1999 (first entry)

DE BCL2-targeted antisense oligonucleotide SEQ ID NO:45.

KW Combinatorial antisense library; oligonucleotide analogue; RNase;
KM ribozyme; cleavage; anchor; binding; target RNA; ss.

XX Synthetic.

OS WO9118238-A1.

PN 15-APR-1999.

PD 28-SEP-1998; 98WO-US20361.

PR 18-AUG-1998; 98US-0136080.

XX 02-OCT-1997; 97US-0060673.

PA (OASIS-) OASIS BIOSCIENCES INC.

PI Arnold LJ, Brown BD, Riley TA;

DR WPI; 1999-264039/22.
XX
PT oligonucleotide analog compositions capable of coupling to form
XX antisense molecules

PS Example 9; Page 45; 71pp; English.

CC The present invention describes a composition comprising two
CC oligonucleotide analogues, each having a binding domain and a coupling
CC moiety, where the binding domains are capable of hybridizing to a target
CC polynucleotide and the coupling moieties are capable of coupling to each
CC other in the absence of a target molecule. The composition/compound is
CC used to cleave an RNA target. The compositions can be used to determine
CC an optimal antisense site for a given mRNA or an optimal ribozyme
CC cleavage site for a target RNA. By separating the antisense molecules
CC into two or more pieces, a comprehensive antisense library can be
CC prepared in advance, rather than synthesizing a plurality of candidate
CC antisense molecules as needed. A complete library of every possible
CC 17-mer oligonucleotide, using the four natural bases, would consist of
CC 417 (or about 1.7 x 10¹⁰) molecules. By providing the antisense molecules
CC in at least two components, e.g. a library of 8-mers and a library of
CC 9-mers, assembled quickly as needed, the library size is reduced to 48 +
CC 49, or 327 650 molecules. The complexity of the library can be further
CC reduced by substituting one or more universal or degenerate bases for
CC some of the natural bases. The present sequence represents an
CC oligonucleotide, which is used in an example from the present invention.
XX

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccagcgtgcgcacat 18
Db 1 tctccagcgtgcgcacat 18

RESULT 12

AAK33693
ID AAK33693 standard; DNA; 18 BP.

XX AAK33693;

DT 18-JUN-1999 (first entry)

DE Deletion sequence oligonucleotide 146.

KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.

XX Synthetic.

OS WO911820-A1.

PN 11-MAR-1999.

PD 01-SEP-1998; 98WO-US18084.

PR 02-SEP-1997; 97US-0923771.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Srivatsa GS;

XX WPI; 1999-205198/17.

DR
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides

PS Example 9; Page 152; 163pp; English.

CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAK33548-X23709.
CC compositions that are useful for modulating cellular pharmaceutical
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, including influenza virus (HIV), or a non-human
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 13
AAK27536/c
ID AAK27536 standard; RNA; 18 BP.

AC AAK27536;

DT 27-MAY-1999 (first entry)

DE Synthetic RNA sequence produced by the method of the invention.

XX Sillyoxymethyl phosphonate; sillyoxymethyl halide; diagnosis; ss;
KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.

XX Synthetic.

XX WO9909044-A1.

XX 25-FEB-1999.

XX 17-AUG-1998; 98WO-EP05215.

XX 18-AUG-1997; 97CH-0001931.

XX (JENN/) JENNY L.
PA (PITS/) PITTSCH S.
PA (WEIS/) WEISS P. A.

PI Jenny L, Pitsch S, Weiss PA;

DR WPI, 1999-180963/15.

XX 2-sillyoxymethyl ribonucleosides and their phosphonate derivatives
PT - have high purity, use in machine synthesis of ribonucleic acids,
PR enable longer oligonucleotide chain construction, and larger amounts

XX Example 7; Page 26; 38pp; English.

XX The invention relates to sillyoxymethyl protected D- or L-ribonucleosides
CC and their phosphonates (I), and sillyoxymethyl halides (II). (I) are
CC intermediates for synthesis of RNA-oligonucleotides with predetermined
CC nucleotide sequence, particularly by machine synthesis. The groups
CC specified above, apart from those on silly, are those particularly for
CC the cyanoethyl phosphoramidate coupling. Uses of the oligonucleotide
CC products in diagnosis, therapy, and as research tools, are well known,
CC and are not dealt with in detail. (II) is an intermediate for (I). The
CC sillyoxymethyl halide reagent is easy to prepare, and yields are high.
CC Introduction of the sillyoxymethyl group into the ribonucleoside is
CC simple and rapid, and the acetal bond formed does not migrate,
CC eliminating particularly the prior art problem of 2' to 3' isomerisation.
CC The methylenedioxy group spacer between the silly group and nucleoside
CC ring results in less steric hindrance than bulky direct sillyoxy
CC linkages, enabling firstly, a range of choices for the silly substituents,
CC to provide, e.g., acid or base stability; and second, higher yields in
CC coupling. Purer products are therefore obtained than in prior art,
CC enabling larger quantities and longer chains of oligoribonucleotides to
CC be synthesised successfully, and in shorter times.

XX Sequence 18 BP; 4 A; 4 C; 8 G; 2 U; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 18 tctccagcgtgcgcacat 1

RESULT 14
AAK18702
ID AAK18702 standard; DNA; 18 BP.

AC AAK18702;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide BCL-2.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
KW alimentary canal; transport; gastrointestinal mucosa; cancer;
KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
KW HIV; inflammation; ss.

XX Synthetic.

XX WO9901579-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13574.

XX 01-JUL-1997; 97US-0886829.

XX (ISIS-) ISIS PHARM INC.

PI Hardee G, Teng C;

DR WPI, 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used
PT particularly for delivering therapeutic antisense oligonucleotides
PR across the gastrointestinal mucosa, provides high bioavailability
XX Example 2; Page 86; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35%. The penetration enhancer improves: (i) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAK18669 to AAK18799 and AAK18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 15
AAV99434

Search completed: June 28, 2002, 22:40:21
Job time: 8097 sec

ID AAV99434 standard; DNA; 18 BP.
XX
AC AAV99434;
XX
DT 22-MAR-1999 (first entry)
XX
DE Antisense oligonucleotide directed against human bcl-2 gene.
XX
KW Antisense oligonucleotide: human bcl-2 gene; phosphorothioate;
KW phosphodiester: lipid-encapsulation; tumour; aberrant gene expression;
KW treatment; inflammation; infection; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FH modified_base 1..18
FT /tag= a
FT /note= "phosphorothioate or phosphodiester bonds"
XX
PN WO9851278-A2.
XX
PD 19-NOV-1998.
XX
PF 14-MAY-1998: 98WO-CA00485.
XX
PR 14-MAY-1997: 97US-0856374.
XX
PA (INEX-) INEX PHARM CORP.
XX
PI Ansel SM, Cullis P, Debeyer D, Harasym T, Hope MJ;
PI Klimuk SK, Scherrer P, Semple SC;
XX
DR WPI: 1999-045179/04.
XX
PT Composition containing lipid-encapsulated therapeutic agent -
PT useful, e.g. for delivering antisense molecules or ribozymes or
PT treating diseases associated with aberrant gene expression
XX
PS Disclosure: Page 23: 98pp; English.
XX
CC The present sequence represents an antisense oligonucleotide directed
CC against the human bcl-2 gene. The oligonucleotide can have either
CC phosphorothioate or phosphodiester bonds. The oligonucleotide is
CC lipid-encapsulated using the method of the invention. A composition
CC comprising lipid-encapsulated particles of a therapeutic agent,
CC e.g. antisense oligonucleotides, is prepared by mixing at least
CC 2 lipids with buffered aqueous solution of charged therapeutic
CC agent to form an intermediate mixture of lipid-encapsulated particles,
CC and changing the pH of the mixture to neutralise at least some of the
CC external surface charges on the particles. One lipid has a
CC (de)protonatable group with Ka such that the lipid is charged at a
CC first pH but neutral at a second pH (particularly near physiological pH)
CC and the buffer maintains this lipid in the charged form (i.e. cationic
CC when the therapeutic agent is anionic in the buffer, or vice versa). The
CC second lipid prevents particle aggregation during formation of the
CC lipid-therapeutic agent particles. The composition is used to introduce
CC therapeutic agents into cells, in vivo or in vitro, particularly to
CC treat or prevent diseases associated with aberrant gene expression in
CC mammals, specifically tumours, inflammation or infection.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 18; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. NO. 6.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
DB 1 tctccagcgtgcgcacat 18

Mon Jul 1 08:40:52 2002

us-09-709-170a-17.szm75.rng

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:53 ; Search time 334.55 Seconds
(without alignments)
13.216 Million cell updates/sec

Title: US-09-709-170A-17

Sequence: 1 tctccagcgtcgccat 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, NA:*

1: /cgn2_6/prodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/prodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/prodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/prodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/prodata/1/lna/PCITUS.COMB.seq:*
6: /cgn2_6/prodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	1	US-08-217-082A-17
2	18	100.0	18	2	US-08-465-485A-17
3	18	100.0	18	2	US-08-465-485A-24
4	18	100.0	18	3	US-09-080-285-17
5	18	100.0	18	3	US-09-080-285-24
6	18	100.0	18	3	US-09-249-730-218
7	18	100.0	18	3	US-09-118-220-1
8	18	100.0	18	4	US-08-738-652-55
9	18	100.0	18	4	US-09-030-701-27
10	18	100.0	18	4	US-09-286-098-59
11	18	100.0	18	4	US-08-286-098-104
12	18	100.0	18	4	US-08-960-774-45
13	18	100.0	18	4	US-09-078-934-14
14	18	100.0	20	4	US-09-082-649B-60
15	18	100.0	20	4	US-08-410-804-13
16	18	100.0	27	1	US-08-607-269-8
17	18	100.0	27	1	US-08-259-514-13
18	18	100.0	27	1	US-08-858-311-13
19	18	100.0	27	2	US-08-858-311-13
20	18	100.0	27	5	PCT-US95-04600-8
21	18	100.0	35	1	US-08-217-082A-2
22	18	100.0	35	2	US-08-465-485A-2
23	18	100.0	35	3	US-09-080-285-2
24	18	100.0	17	1	US-08-217-082A-9
25	16.4	91.1	18	4	US-09-030-701-41
26	16.4	91.1	18	4	US-09-030-701-60
27	16.4	91.1	18	4	US-09-286-098-72
			4		US-08-960-774-72

28	16.4	91.1	20	4	US-09-109-663-72	Sequence 72, Appl
29	15.4	85.6	33	3	US-08-650-726-1	Sequence 1, Appl
30	15	83.3	17	1	US-08-217-082A-8	Sequence 8, Appl
31	15	83.3	17	2	US-08-877-831-1	Sequence 1, Appl
32	14	77.8	17	1	US-08-217-082A-10	Sequence 10, Appl
33	13.8	76.7	31	1	US-08-726-136-19	Sequence 19, Appl
34	13.8	76.7	31	3	US-09-103-434-19	Sequence 19, Appl
35	13.8	76.7	31	3	US-09-687-594-19	Sequence 19, Appl
36	13.4	74.4	17	4	US-08-030-701-40	Sequence 40, Appl
37	13.4	74.4	17	4	US-09-286-098-71	Sequence 71, Appl
38	13.4	74.4	17	4	US-08-960-774-71	Sequence 71, Appl
39	13	72.2	20	1	US-08-217-082A-1	Sequence 1, Appl
40	13	72.2	20	1	US-08-217-082A-7	Sequence 7, Appl
41	13	72.2	20	2	US-08-465-485A-1	Sequence 1, Appl
42	13	72.2	20	2	US-08-465-485A-7	Sequence 7, Appl
43	13	72.2	20	3	US-09-080-285-1	Sequence 1, Appl
44	13	72.2	20	3	US-09-080-285-7	Sequence 7, Appl
45	13	72.2	20	4	US-09-379-718-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-217-082A-17
Sequence 17, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Forthney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
US-08-217-082A-17

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccacgctgcccacat 18
Db 1 TCTCCACGCTGCCCAT 18

RESULT 2
US-08-465-485A-17
Sequence 17, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Portney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-485A-17

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccacgctgcccacat 18
Db 1 TCTCCACGCTGCCCAT 18

RESULT 3
US-08-465-485A-24
Sequence 24, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:

APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Portney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 16..17
OTHER INFORMATION: Last two internucleoside linkages are
phosphorothioates
US-08-465-485A-24

Query Match 100.0%; Score 18; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccacgctgcccacat 18
Db 1 TCTCCACGCTGCCCAT 18

RESULT 4
US-09-080-285-17
Sequence 17, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/080,285
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/465,485
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/124,256
 FILING DATE: 20-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/840,716
 FILING DATE: 21-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/288,692
 FILING DATE: 22-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fortney, Andrew D.
 REGISTRATION NUMBER: 34,600
 REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 436-2070
 TELEFAX: (408) 436-2075
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-080-285-17

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;
 QY 1 tctccagctgagccat 18
 ||||||||||||
 DB 1 TCTCCAGCTGCGCCAT 18

RESULT 5
 US-09-080-285-24
 ; Sequence 24, Application US/09080285
 ; Patent No. 6040181
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John
 ; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ; ADDRESS: P.C.
 ; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: U.S.A.
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentln Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/465,485
 FILING DATE: 05-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/124,256
 FILING DATE: 20-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/840,716
 FILING DATE: 21-FEB-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/288,692
 FILING DATE: 22-DEC-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: Fortney, Andrew D.
 REGISTRATION NUMBER: 34,600
 REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (408) 436-2070
 TELEFAX: (408) 436-2075
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid;
 DESCRIPTION: Synthetic DNA
 ANTI-SENSE: YES
 FEATURE:
 NAME/KEY: Modified_base
 LOCATION: 16..17
 OTHER INFORMATION: Last two internucleoside linkages are
 OTHER INFORMATION: phosphorothioates
 US-09-080-285-24

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;
 QY 1 tctccagctgagccat 18
 ||||||||||||
 DB 1 TCTCCAGCTGCGCCAT 18

RESULT 6
 US-09-249-730-218
 ; Sequence 218, Application US/09249730
 ; Patent No. 6121000
 ; GENERAL INFORMATION:
 ; APPLICANT: WRIGHT, Jim A.
 ; TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
 ; FILE REFERENCE: 032396-040
 ; CURRENT APPLICATION NUMBER: US/09/249,730
 ; CURRENT FILING DATE: 1999-02-11
 ; NUMBER OF SEQ ID NOS: 220
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 218
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-249-730-218

Query Match 100.0%; Score 18; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.4; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

QY 1 tctccagcgtgcgcacat 18
|||||
Db 1 tctccagcgtgcgcacat 18

RESULT 7

US-09-118-220-1
; Sequence 1, Application US/09118220
; Patent No. 6140051
; GENERAL INFORMATION:
; APPLICANT: Brown, Lauren R.
; APPLICANT: Xu, Cheng
; TITLE OF INVENTION: FLUORESCENT DIBENZAZOLE DERIVATIVES
; TITLE OF INVENTION: AND METHODS RELATED THERETO
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive, 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/118,220
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartfield, Neil S
; REGISTRATION NUMBER: 39,901
; REFERENCE/DOCKET NUMBER: GENTA.050A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-118-220-1

Query Match 100.0%; Score 18; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctccagcgtgcgcacat 18
|||||
Db 1 tctccagcgtgcgcacat 18

RESULT 8

US-08-738-652-55
; Sequence 55, Application US/08738652B
; Patent No. 6207646
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules
; FILE REFERENCE: C1039/7004 HCL
; CURRENT APPLICATION NUMBER: US/08/738,652B
; CURRENT FILING DATE: 1996-10-30
; EARLIER APPLICATION NUMBER: US 08/276,358
; EARLIER FILING DATE: 1994-07-15

; EARLIER APPLICATION NUMBER: US 08/386,063
; EARLIER FILING DATE: 1995-02-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-08-738-652-55

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctccagcgtgcgcacat 18
|||||
Db 1 tctccagcgtgcgcacat 18

RESULT 9

US-09-030-701-27
; Sequence 27, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; FILE REFERENCE: C1039/7011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-27

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tctccagcgtgcgcacat 18
|||||
Db 1 tctccagcgtgcgcacat 18

RESULT 10

US-09-286-098-59
; Sequence 59, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-59

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 11
US-09-286-098-104
Sequence 104, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:
APPLICANT: Krieger, Arthur M.
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
TITLE OF INVENTION: Cytokines
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286,098
CURRENT FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 104
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-104

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 12
US-08-960-774-45
Sequence 45, Application US/08960774
Patent No. 6239116
GENERAL INFORMATION:
APPLICANT: Krieger et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.,
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-960-774-45

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 tctccagcgtgcgcacat 18

RESULT 13
US-09-078-954-14
Sequence 14, Application US/09078954
Patent No. 6287591
GENERAL INFORMATION:
APPLICANT: SEMPLER, Sean C.
APPLICANT: Klimuk, Sandra K.
APPLICANT: Harasym, Troy
APPLICANT: Hope, Michael J.
APPLICANT: Ansell, Steven M.
APPLICANT: Cullis, Pieter
APPLICANT: Scherrer, Peter
APPLICANT: Geisler, Timothy
APPLICANT: Zon, Gerald
APPLICANT: Debever, Dan
TITLE OF INVENTION: High Efficiency Encapsulation of Charged Therapeutic Agents
TITLE OF INVENTION: Lipid Vesicles
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,954
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,374
FILING DATE: 14-MAY-1997
ATTORNEY/AGENT INFORMATION:

NAME: Marina T. Larson
REGISTRATION NUMBER: 32,038
REFERENCE/DOCKET NUMBER: INEX.P-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
TELEFAX: (970) 668-2082
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 18
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHEICAL: no
ANTI-SENSE: yes
US-09-078-954-14

Query Match 100.0%; Score 18; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 TCTCCAGCGTGCGCCAT 18

RESULT 14
US-09-082-649B-60
Sequence 60, Application US/09082649B
Patent No. 633068
GENERAL INFORMATION:
APPLICANT: Davis, Heather L.
APPLICANT: Krieger, Arthur M.
APPLICANT: Schorr, Joachim
APPLICANT: Wu, Tong
TITLE OF INVENTION: Vectors and Methods for Immunization or
FILE REFERENCE: C1039/7008
CURRENT APPLICATION NUMBER: US/09/082,649B
PRIOR FILING DATE: 1998-05-20
PRIOR APPLICATION NUMBER: US 60/047,233
PRIOR FILING DATE: 1997-05-20
PRIOR APPLICATION NUMBER: US 60/047,209
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 85
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-082-649B-60

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 1 TCTCCAGCGTGCGCCAT 18

RESULT 15
US-08-410-804-13/C
Sequence 13, Application US/08410804
Patent No. 5632994
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaaki

TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-410-804-13

Query Match 100.0%; Score 18; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
|||||
DB 25 TCTCCAGCGTGCGCCAT 8

Search completed: June 28, 2002, 22:16:53
Job time: 8279 sec

Mon Jul 1 08:40:52 2002

us-09-709-170a-17.szlm75.rni

Query Match	100.08;	Score 16;	DB 6;	Length 16,
Best Local Similarity	100.08;	Pred. No. 1.2e+04;		

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

DB 1 CGGAGCGCGCGCGCC 16

RESULT 2
AR032762/c
LOCUS AR032762
DEFINITION Sequence 374 from patent US 5869241.
ACCESSION AR032762
VERSION AR032762.1 GI:5948367
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Method of determining DNA sequence preference of a DNA-binding molecule
JOURNAL Patent: US 5869241-A 374 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"

BASE COUNT 0 a 34 c 13 g 3 t
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

DB 43 CGGAGCGCGCGCGCC 28

RESULT 3
LOCUS 129502
DEFINITION Sequence 374 from patent US 5578444.
ACCESSION 129502
VERSION 129502.1 GI:1820293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
TITLE Sequence-directed DNA-binding molecules compositions and methods
JOURNAL Patent: US 5578444-A 374 26-NOV-1996;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"

BASE COUNT 0 a 34 c 13 g 3 t
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

DB 43 CGGAGCGCGCGCGCC 28

RESULT 4
LOCUS 191176
DEFINITION Sequence 374 from patent US 5726014.
ACCESSION 191176

50 bp DNA linear PAT 01-DEC-1998

VERSION 191176.1 GI:3935646
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)
AUTHORS Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
TITLE Screening assay for the detection of DNA-binding molecules
JOURNAL Patent: US 5726014-A 374 10-MAR-1998;
FEATURES Location/Qualifiers
source 1..50
/organism="unknown"

BASE COUNT 0 a 34 c 13 g 3 t
ORIGIN

Query Match 100.0%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

DB 43 CGGAGCGCGCGCGCC 28

RESULT 5
LOCUS AX008888
DEFINITION Sequence 3 from Patent WO9964584.
ACCESSION AX008888
VERSION AX008888.1 GI:996309
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 35)
AUTHORS Kramer,P. and Peter,M.
TITLE Protein for regulating apoptosis
JOURNAL Patent: WO 9964584-A 3 16-DEC-1999;
FEATURES Location/Qualifiers
source 1..35
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 6 a 10 c 16 g 3 t
ORIGIN

Query Match 80.0%; Score 12.8; DB 6; Length 35;
Best Local Similarity 87.5%; Pred. No. 2.1e+05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcgcc 16
|||||

DB 9 CGGAGCATGCGCGCC 24

RESULT 6
LOCUS 567824
DEFINITION 53 bp DNA linear VRL 23-SEP-1994
envelope protein p43K [promoter] [Molluscum contagiosum virus subtype II MCV II, Genomic, 53 nt].
ACCESSION 567824
VERSION 567824.1 GI:544609
KEYWORDS
SOURCE Molluscum contagiosum virus subtype 2.
ORGANISM Molluscum contagiosum virus subtype 2.
REFERENCE 1 (bases 1 to 53)
AUTHORS Porter,C.D., Blake,N.W., Cream,J.J. and Archard,L.C.
TITLE Molluscum contagiosum virus

JOURNAL
MoL. Cell Biol. Hum. Dis. Ser. 1, 233-257 (1992)
MEDLINE
9408453
REMARK
entry [NCBI q1bbssr 142099] from the original journal article.
MoL. Cell Biol. Hum. Dis. Ser. 1, 233-257 (1992)

FEATURES	location/Qualifiers
source	1..53
	location:="Molluscum contagiosum virus subtype 2"

gene 51. :53 /partial

BASE COUNT	6 a	15 c	22 g	10 t
ORIGIN	/gene="envelope protein p43"			

Query Match	80.0%	Score 12.8	DB 14	Length 53
Best Local Similarity	87.5%	Pred. No. 1.9e+05		
Matches 14; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy	1	cgagagcgcgcgcgcgc	16
Db	1	CGGCGCGCGGCTGGC	16

LOCUS	17 bp	mrna	linear	PAT 07-SEP-2001
AX215485/c				
LOCUS	AX215485			
DEFINITION	Sequence 927 from Patent WO0159103.			
ACCESSION	AX215485			
VERSION	AX215485.1	GI:1552528		

REFERENCE	AUTHORS	TITLE
1 (cases 1 to 17)	Blatt, L., Mcswigen, J. and Chowrira, B. M.	Method and reagent for the modulation and diagnosis of cd20 and

FEATURES	location/Qualifiers
source	1..17
	/db_organism="synthetic construct"
	/db_xref="taxon:32630"
	/note="Nucleic Acid"
BASE COUNT	0 a 12 c 4 g 1 t
ORIGIN	

	Query Match:	77.5%;	Score 12.4;	DB 6;	length 17;
	Best Local Similarity	92.9%;	Pred. No. 3.7e+05;		
	Matches 13;	Conservative	0;	Mismatches 1;	Indels 0;
QY	2	gggagcgcgagcgag	15		
Db	17	GGGGGCGCGGGGG	4		

RESULT	8		
AX216149/c			
LOCUS	AX216149	17 bp	mRNA
DEFINITION	Sequence 1591 from Patent WO0159103.		linear
ACCESSION	AX216149		
VERSION	AX216149.1	GI:15526192	
KEYWORDS			
SOURCE			
	synthetic construct.		

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 17)	Blatt, L., McSwiggen, J. and Chowrira, B.M.	Method and reagent for the modulation and diagnosis of cd20 and

JOURNAL	patent: WO 0159103-A 1591 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowritra, Bharat M. (US)
FEATURES	Location/Qualifiers
source	1..17
	/organism="synthetic construct" /db_xref="taxon:32630" /note="Nucleic Acid"
BASE COUNT	0 a 13 c 3 g 1 t
ORIGIN	

Query Match	77.5%;	Score 12.4;	DB 6;	Length 17;
Best Local Similarity	92.9%;	Pred. No. 3.7e+05;		
Matches 13; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY 2 gggaagcgcgcggg 15
||| |||||
Db 16 GGGGGCGCGCGG 3

RESULT	9	17 bp	MRNA	linear	PAT 07-SEP-2001
AX216150/c	AX216150				
LOCUS					
DEFINITION	Sequence 1592 from Patent WO0159103.				
ACCESSION	AX216150				
VERSION	AX216150.1	GI:15526193			
KEYWORDS					

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 17)
Blatt, L., McSwigen, J. and Chowrira, B. M.
Method and reagent for the modulation and diagnosis of cd20 and
novo gene expression
Patent: WO 0159103-A-1592 16-AUG-2001;
RIBOTYME PHARMACEUTICALS, INC.; Blatt, Lawrence (US);
McSwigen, James (US); Chowrira, Bharat M. (US)

```

source      1. .17
             /organism="synthetic construct"
             /db_xref="taxon:32630"
             /note="Nucleic Acid"
BASE COUNT  0 a      13 c      3 g      1 t
ORIGIN

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	Query Match	Score 12.4	DB 6	Length 17
Best Local Similarity	92.9%	Pred: No. 3	7e+05	
Matches 11; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	2	ggagagcgcgcgcg	15	
Db	14	ggggcgcgcgcgcg	1	

RESULT	10		
LOCUS	AR139322/c	20 bp	DNA
DEFINITION	AR139322		linear
ACCESSION	Sequence 30 from patent US 6207372.		PAT 16-JUN-2001
VERSION	AR139322.1	GI:14481818	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 20)		
	Shuber A.P.		

REFERENCE	1 (bases 1 to 20)
AUTHORS	Shuber, A.P
TITLE	Universal primer sequence for multiplex DNA amplification
JOURNAL	Patent: US 6207372-A 30 27-MAR-2001;
FEATURES	location/Qualifiers
SOURCE	1..20

BASE COUNT 0 a 14 c 6 g 0 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 20;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 ggaagcgcgcgcgc 16
15 GGGGGCGGGCGGC 2

RESULT 11
LOCUS AR003393/c 21 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 28 from patent US 5744306.
ACCESSION AR003393
VERSION AR003393.1 GI:3964652
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Murtagh,J.J., Jr. and Thunnissen,F.B.J.M.
TITLE Methods for nucleic acid detection, sequencing, and cloning using
exonuclease
JOURNAL Patent: US 5744306-A 28 28-APR-1998;
FEATURES
source 1..21
Location/Qualifiers
BASE COUNT 0 a 15 c 6 g 0 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 ggaagcgcgcgcgc 16
15 GGGGGCGGGCGGC 2

RESULT 12
LOCUS I21182/c 21 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 28 from patent US 5518901.
ACCESSION I21182
VERSION I21182.1 GI:1601536
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Murtagh,J.J.
TITLE Methods for adapting nucleic acid for detection, sequencing, and
cloning using exonuclease
JOURNAL Patent: US 5518901-A 28 21-MAY-1996;
FEATURES
source 1..21
Location/Qualifiers
BASE COUNT 0 a 15 c 6 g 0 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 ggaagcgcgcgcgc 16
15 GGGGGCGGGCGGC 2

Db 15 GGGGGCGGGCGGC 2

RESULT 13
LOCUS I74449/c 21 bp DNA linear PAT 03-APR-1998
DEFINITION Sequence 28 from patent US 5688669.
ACCESSION I74449
VERSION I74449.1 GI:3010590
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 21)
AUTHORS Murtagh,J.J.
TITLE Methods for nucleic acid detection, sequencing, and cloning using
exonuclease
JOURNAL Patent: US 5688669-A 28 18-NOV-1997;
FEATURES
source 1..21
Location/Qualifiers
BASE COUNT 0 a 15 c 6 g 0 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 21;
Best Local Similarity 92.9%; Pred. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 3 ggaagcgcgcgcgc 16
15 GGGGGCGGGCGGC 2

RESULT 14
LOCUS AX249410 31 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 1489 from Patent WO0166800.
ACCESSION AX249410
VERSION AX249410.1 GI:15864033
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 31)
AUTHORS Gargill,M., Ireland,V.S. and Lander,E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0166800-A 1489 13-SEP-2001;
FEATURES
source 1..31
Location/Qualifiers
BASE COUNT 2 a 9 c 16 g 3 t 1 others
ORIGIN /db_xref="taxon:9606"

Query Match 77.5%; Score 12.4; DB 6; Length 31;
Best Local Similarity 81.2%; Pred. No. 3.2e+05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 1 cgaagcgcgcgcgc 16
2 CGGAGCGGGGTGKC 17

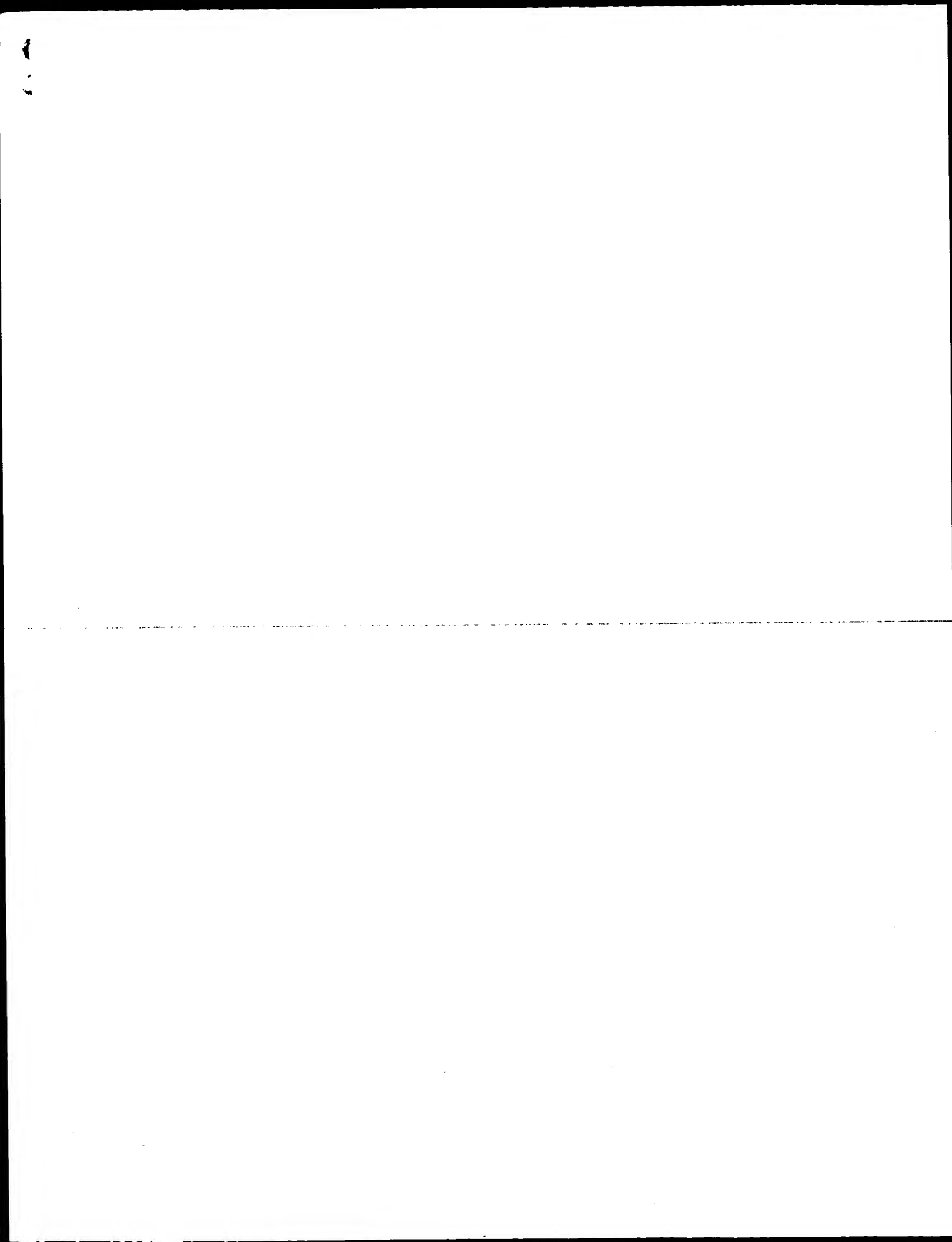
RESULT 15
LOCUS A51123/c 50 bp DNA linear PAT 10-MAR-1997
DEFINITION Sequence 1 from Patent WO9617081.
ACCESSION A51123
VERSION A51123.1 GI:2303898

KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
REFERENCE unclassified.
1 (bases 1 to 50)
AUTHORS Collier,D. and Kerwin,R.
TITLE ASSESSMENT FOR TREATMENT WITH NEUROLEPTIC AGENTS
JOURNAL Patent: WO 9617081-A 1 06-JUN-1996;
INST OF PSYCHIATRY (GB)
COMMENT Other publication AU 3931295 960619.
FEATURES Location/Qualifiers
1. .50
source
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 3 a 25 c 13 g 9 t
ORIGIN

Query Match 77.5%; Score 12.4; DB 6; Length 50;
Best Local Similarity 92.9%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ggagcgcggggggc 16
||| ||||| ||||| |||||
Db 15 ggagcgcggggggc 2

Search completed: June 28, 2002, 22:11:18
Job time: 8369 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Run on:      June 28, 2002, 22:40:19 ; Search time 1381.16 Seconds
              (without alignments)
              19.890 Million cell updates/sec
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Title:	US-09-709-170A-16
Perfect score:	16
Sequence:	1 cggagcgcgcgcgcgc 16

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

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Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 1996432
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Minimum DB seq length: 0
Maximum DB seq length: 75
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post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	100.0	16	16	AA086658	Bcl-2 antisense 01
2	16	100.0	16	19	AAV28180	Antisense oligonucleotide
3	16	100.0	16	20	AAZ23692	Deletion sequence
4	16	100.0	16	20	AAI18701	Target bcl-2 antisense
5	16	100.0	50	15	AA069624	Human bcl-2 proto-oncogene
6	16	100.0	50	18	AAAT64086	Human B-cell leukemia
7	16	100.0	50	20	AAAI7374	Test sequence from human
8	13.6	85.0	65	21	AAAC31547	Human secreted protein
9	13.4	83.8	67	21	AAAI1202	Human secreted protein

C 10	12.8	80.0	25	17	AA42053	Exotoxin A gene PC
C 11	12.8	80.0	31	22	AA131001	Human single nucle
C 12	12.8	80.0	35	21	AA283925	Human DEDD PCR p
C 13	12.8	80.0	38	12	AA044201	Probe p1672 for Gi
C 14	12.8	80.0	47	20	AA052519	PCR primer for in
C 15	12.8	80.0	47	22	AA272719	Human PRO polypept
C 16	12.8	80.0	47	22	AA297500	Human PRO258 in si
C 17	12.8	80.0	71	19	AAV61402	Mouse Clock gene e
C 18	12.8	80.0	71	19	AAV61402	IGF-I oligonucleot
C 19	12.4	77.5	15	22	AAE9184	IGF-I oligonucleot
C 20	12.4	77.5	17	23	ABK00927	Human NOG0 Inocyte
C 21	12.4	77.5	17	23	ABK01591	Human NOG0 G-Cleav
C 22	12.4	77.5	17	23	ABK01592	Human NOG0 G-Cleav
C 23	12.4	77.5	20	18	AA474733	Variant #29 of unl
C 24	12.4	77.5	21	16	AA078562	Gene-specific prim
C 25	12.4	77.5	21	16	AA180851	Gene-specific prim
C 26	12.4	77.5	24	21	AA228432	PCR primer Jc171 f
C 27	12.4	77.5	33	21	AAA60889	Mouse cystatin C p
C 28	12.4	77.5	40	17	AA03676	Hepatitis C diagno
C 29	12.4	77.5	47	18	AAAT73790	Multiplex short-PC
C 30	12.4	77.5	49	18	AAAT73806	Multiplex short-PC
C 31	12.4	77.5	49	18	AAAT73786	Multiplex short-PC
C 32	12.4	77.5	50	17	AAAT28823	PCR primer for HMR
C 33	12.4	77.5	50	18	AAAT73798	Multiplex short-PC
C 34	12.4	77.5	50	18	AAAT73801	Multiplex short-PC
C 35	12.4	77.5	50	18	AAAT73804	Multiplex short-PC
C 36	12.4	77.5	50	18	AAAT73781	Multiplex short-PC
C 37	12.4	77.5	50	18	AAAT73782	Multiplex short-PC
C 38	12.4	77.5	50	18	AAAT73788	Multiplex short-PC
C 39	12.4	77.5	50	18	AAAT73770	Multiplex short-PC
C 40	12.4	77.5	50	18	AAAT73774	Multiplex short-PC
C 41	12.4	77.5	50	18	AAAT73766	Multiplex short-PC
C 42	12.4	77.5	50	18	AAAT73762	Multiplex short-PC
C 43	12.4	77.5	50	18	AAAT73764	Multiplex short-PC
C 44	12.4	77.5	50	22	AA130181	Human SNP oligonuc
C 45	12.4	77.5	50	22	AA134074	Human SNP oligonuc

ALIGNMENTS

RESULT	1
AAQ86658	
ID	AAQ86658 standard; DNA; 16 BP.

DT 27-SEP-1995 (first entry)

Bcl-2 antisense oligonucleotide.

Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW Lymphoma; programmed cell death; ss

05 Synthetic.

XX	Key	Location/Qualifiers
FH		

misc_feature

	antisense	sense
L1	-0.68	-0.79
ET	-0.68	-0.79

/note= "3'-5' (antisense) sequence"

XX
XX
PN W09508350-A

XX
XX
30-MAP-1995

XX
0450 F01073E

XX

XX
PR 20-BFF-1999,
XX

PA (REED/)
yy

PI

DR WPI: 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086550-55) or the 5'-cap
CC region (AA086556-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 16 BP; 1 A; 5 C; 10 G; 0 T; 0 other;

Query Match 100.0%; Score 16; DB 16; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cggagagcgcgcgcggc 16
|||||
Db 1 cggagagcgcgcgcggc 16

RESULT 2

AAV28180
ID AAV28180 standard; DNA; 16 BP.

AC AAV28180;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

XX MO9827425-A1.

PN 25-JUN-1998.

PD 18-DEC-1997; 97WO-US3284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI: 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,
e.g. large scale purification of anti-sense agents from their
deletion derivatives formed during synthesis

PS Disclosure; Page 85; 183pp; English.

AAV28180-268 represent oligonucleotides which can be purified using the
method of the invention. The specification describes a matrix that
comprises a support and an affinity unit that specifically and
reversibly binds a target oligonucleotide, and comprises a sequence of
bases having the reverse complement of a hybridizing portion of the
target oligonucleotide. The matrix is used for affinity purification of
synthetic oligonucleotides, specifically antisense agents, for treatment
of hyperproliferative diseases, for treating a non-pathogen,
non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
expression of cell surface proteins, and to inhibit a eukaryotic
pathogen, retrovirus or other viruses.

Sequence 16 BP; 1 A; 5 C; 10 G; 0 U; 0 other;

Query Match 100.0%; Score 16; DB 19; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgcgcgcggc 16
|||||
Db 1 cggagagcgcgcgcggc 16

RESULT 3

AAV23692
ID AAV23692 standard; DNA; 16 BP.

AC AAV23692;

DT 18-JUN-1999 (first entry)

DE Deletion sequence oligonucleotide 145.

KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;

KW probe; cellular adhesion modulator; cellular proliferation modulator;

KW human retrovirus; human immunodeficiency virus; non-human retrovirus;

KW HIV; primer; ss.

OS Synthetic.

XX WO9911820-A1.

PN 11-MAR-1999.

PD 01-SEP-1998; 98WO-US18084.

PR 02-SEP-1997; 97US-0923771.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Srivatsa GS;

DR WPI: 1999-205198/17.

PT New compositions comprising sensor arrays made up of unique probe
oligonucleotides - useful for characterizing a sample of target
deletion oligonucleotides

PS Example 9; Page 152; 163pp; English.

This invention describes a novel composition comprising a number of
sensor arrays, where each array comprises a unique probe
oligonucleotide, which is the reverse complement of part of a unique
target oligonucleotide present in a mixture of target deletion sequence
oligonucleotides. The compositions form a method for characterizing a
sample of target deletion oligonucleotides which are labeled and
hybridize with the probe oligonucleotides of the sensor arrays. Such
oligonucleotides and their targets are represented in AAV23348-X23709.
Compositions that are useful for modulating cellular adhesion or
proliferation, and being active against a eukaryotic pathogen, a human
retrovirus, a human immunodeficiency virus (HIV), or a non-human
retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
Syncytial Virus or cytomegalovirus (CMV). The compositions enable
characterization of deletion sequence oligonucleotides having related,
but different nucleobase sequences, and quantification of different
species of deletion sequence ("target") oligonucleotides in a mixture.
Also, if the specificity of the oligonucleotide's nucleobase sequence
for its reverse complement is not modified, the method may be performed
using oligodeoxynucleotides.

Sequence 16 BP; 1 A; 5 C; 10 G; 0 U; 0 other;

Query Match 100.0%; Score 16; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgggagcgcgcgcggc 16
|||||
Db 1 cgggagcgcgcgcggc 16

RESULT 4

AA18701
ID AA18701 standard; DNA; 16 BP.

AC AA18701;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #33.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;

KM Alzheimer's disease; beta-thalassemia; malaria; viral infection;

KW HIV; inflammation; ss.

OS Synthetic.

PN MO9901579-A1.

PD 14-JUN-1999.

PF 01-JUL-1998; 98WO-US13574.

PR 01-JUL-1997; 97US-0886829.

PS (ISIS-) ISIS PHARM INC.

PI Hardee G, Teng C;

PT WPI; 1999-106077/09.

PS Example 2; Page 86; 115pp; English.

A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AA18669 to AA18799 and AA18801 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention.

SO Sequence 16 BP; 1 A; 5 C; 10 G; 0 U; 0 other;

Query Match

Best Local Similarity 100.0%; Score 16; DB 20; Length 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgggagcgcgcgcggc 16
|||||
Db 1 cgggagcgcgcgcggc 16

RESULT 5

AA069624/C
ID AA069624 standard; DNA; 50 BP.

AC AA069624;

DT 01-MAR-1995 (first entry)

DE Human bcl-2 proto-oncogene, target region.

KW DNA protein-binding assay; test sequence; screening sequence;

KM promoter; target; TATA box; Herpes Simplex Virus; HSV;

KW origin of replication; UL9; transcription factor; TRFID; ds.

OS Synthetic.

PN WO9414980-A.

PD 07-JUL-1994.

PF 20-DEC-1993; 93WO-US12388.

PR 23-DEC-1992; 92US-0996783.

PR 17-SEP-1993; 93US-0123936.

PS (GENE-) GENELABS TECHNOLOGIES INC.

PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

PT WPI; 1994-234711/28.

PS Claim 28; Page 399; 587pp; English.

A DNA protein-binding assay is provided, useful for screening libraries of synthetic or biological cpos. For their ability to bind DNA test sequences. The assay is versatile in that any number of test sequences can be tested by placing the test sequence adjacent to a defined protein-binding screening sequence. Binding of mols. to these test sequences changes the binding characteristics of the protein mol. to its cognate binding sequence. When such a mol. binds the test sequence, the equilibrium of the DNA:protein complexes is disturbed, generating changes in the concentration of free DNA probe. One application of this method is to eucaryotic general transcription factors (e.g. TFIID), where the target region is typically selected from DNA sequences adjacent to the binding site for the eucaryotic transcription factor. Numerous exemplary test sequences are given: the sequences in AA069251-731 and AA069850 correspond to promoter targets (typically, TATA box-contg. sites) for human genes and the sequences in AA069732-849 correspond to promoter targets for viral genes. The test sequences may also be randomly generated. DNA:protein interaction may be used for screening purposes, e.g. the Herpes Simplex Virus (HSV) origin of replication and UL9 (see AA069851-52, AA069865 and AA069891).

SO Sequence 50 BP; 0 A; 34 C; 13 G; 3 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 16; DB 15; Length 50;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgggagcgcgcgcggc 16
|||||
Db 43 CGGAGCGCGCGCGGC 28

RESULT 6

AA164086/C
ID AA164086 standard; DNA; 50 BP.

XX AAT64086;
 AC
 XX 14-MAR-1997 (first entry)
 DT
 XX Human B-cell leukemia/lymphoma 2 protooncogene TFIID binding site.
 DE
 XX Duplex DNA; target region; binding characteristic; DNA binding protein;
 KM TFIID; transcription factor; binding site; inhibition; enhance;
 KM cancer; inherited genetic disorder; ds.
 XX
 OS Homo sapiens.
 XX
 PN US5578444-A.
 XX
 PD 26-NOV-1996.
 XX
 PF 27-JUN-1991; 91US-0723618.
 XX
 PR 20-DEC-1993; 93US-0171389.
 PR 27-JUN-1991; 91US-0723618.
 PR 23-DEC-1992; 92US-0996783.
 PR 17-SEP-1993; 93US-0123936.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 DR WPI; 1997-020402/02.
 XX
 PT Altering binding characteristics of DNA binding proteins to duplex
 PT DNA - by attaching specific small cpd. to target region close to the
 PT protein's binding site, useful in treatment of viral disease, cancer
 PT etc
 PS Claim 6; Column 289; 264pp; English.
 XX
 XX The sequences given in AAT63713-4312 represent duplex DNA's which act
 CC as target regions in the method of the invention. The method for
 CC altering the binding characteristics of a DNA-binding protein to duplex
 CC DNA comprises contacting the duplex DNA with a small molecule which
 CC binds sequence-specifically to a target region, where, when the small
 CC molecule is bound to the target region, it is adjacent to, but not
 CC overlapping by more than 4 bp, a binding site for a DNA-binding protein.
 CC The small molecule is added at a concentration effective to alter the
 CC binding of the DNA binding protein, pref. TFIID, to its binding site on
 CC the duplex DNA. The binding of the small molecule may inhibit or
 CC enhance the binding of the DNA-binding protein to its binding site. The
 CC compounds isolated using this method are potentially useful as
 CC therapeutic agents for treatment of any disease which involves a
 CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
 CC The method is suitable for screening large biological or chemical
 CC libraries and allows determination of sequence-specific and relative
 CC affinities of known DNA-binding agents for different DNA sequences.
 CC The design of these duplex DNA's allows a single DNA-protein interaction
 CC to be used for screening sequence-specific, or preferential, DNA binding
 CC proteins that recognise almost any possible sequence (see also AAT95539-
 CC 74).
 XX
 SQ Sequence 50 BP; 0 A; 34 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 16; DB 18; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cggagagcgcgcgagc 16
 |||||
 Db 43 CGGAGAGCGCGCGGCGC 28

RESULT 7
 AAX17374/C

ID AAX17374 standard; DNA; 50 BP.
 XX
 XX AAX17374;
 AC
 XX 06-MAY-1999 (first entry)
 DT
 XX Test sequence from B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene.
 DE
 XX Test sequence; DNA-binding molecule; screening sequence; human;
 KM nucleic acid amplification; target; viral; ds.
 XX
 OS Homo sapiens.
 XX
 PN US5869241-A.
 XX
 PD 09-FEB-1999.
 XX
 PF 07-JUN-1995; 95US-0475228.
 XX
 PR 20-DEC-1993; 93US-0171389.
 PR 27-JUN-1991; 91US-0723618.
 PR 23-DEC-1992; 92US-0996783.
 PR 17-SEP-1993; 93US-0123936.
 PR 07-JUN-1995; 95US-0475228.
 XX
 PA (GENE-) GENELABS TECHNOLOGIES INC.
 XX
 PI Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
 DR WPI; 1999-152755/13.
 XX
 PT Determination of DNA sequence preference of a DNA-binding molecule -
 PT based on inhibition of binding of protein to oligonucleotide
 PT sequence attached to test sequence
 PS Claim 3; Columns 291-292; 270pp; English.
 XX
 XX Sequences AAX17001 to AAX17600 represent specifically claimed target
 CC test sequences that are used in the method of the invention of
 CC determining the DNA sequence preference of a DNA-binding molecule. The
 CC method comprises: (i) adding a test molecule and a DNA-binding protein to
 CC a mixture of duplex DNA test oligonucleotides, each of the test
 CC oligonucleotides having a test sequence adjacent to a screening sequence,
 CC where the screening sequence binds to the DNA-binding protein with a
 CC binding affinity that is independent of the DNA sequence of the test
 CC sequence, and where the mixture of duplex DNA test oligonucleotides
 CC includes several test sequences; (ii) incubating the test molecule, the
 CC mixture of duplex DNA test oligonucleotides and the DNA-binding protein
 CC for a time sufficient to permit binding of the test molecule to test
 CC sequences in the duplex DNA; (iii) separating unbound test
 CC oligonucleotides from test oligonucleotides bound to binding protein;
 CC (iv) amplifying the unbound test oligonucleotides; (v) repeating steps
 CC (ii) to (iv); (vi) isolating the amplified test oligonucleotides; and
 CC (vii) sequencing the isolated test oligonucleotides. Test sequences
 CC AAX17001-X17481 and AAX17600 correspond to promoter targets for human
 CC genes and test sequences AAX17482-X17599 correspond to promoter targets
 CC for viral genes.
 XX
 SQ Sequence 50 BP; 0 A; 34 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 16; DB 20; Length 50;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cggagagcgcgcgagc 16
 |||||
 Db 43 CGGAGAGCGCGCGGCGC 28

RESULT 8
 AAC31547
 ID AAC31547 standard; cDNA; 66 BP.

```

XX AC AAC31547;
XX XX
XX 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 35622.
XX XX
XX KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KM gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PS (GEST ) GENSET.
XX PA Dumas Milne Edwards J, Duclert A, Giordano J;
XX PI WPI; 2000-500381/45.
XX DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS Claim 1; SEQ ID 35622; 71pp + CD-ROM; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors.
XX SQ Sequence 66 BP; 9 A; 27 C; 20 G; 8 T; 2 other;

Query Match 85.0%; Score 13.6; DB 21; Length 66;
Best Local Similarity 81.2%; Pred. No. 3.2e+03;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgggagcgcgcgcg 16
   ||||| ||||| |||||
DB 5 cgggagcgcgcgcg 20

RESULT 9
AAC11202
ID AAC11202 standard; cDNA; 67 BP.
XX AC AAC11202;
XX XX
XX 06-OCT-2000 (first entry)
XX DE Human secreted protein 5' EST, SEQ ID NO: 15277.
XX XX
XX KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KM gene therapy; chromosome mapping; ss.
XX OS Homo sapiens.

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XX PN EP1033401-A2.
XX XX
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-0200610.
XX PR 26-FEB-1999; 99US-0122487.
XX PS (GEST ) GENSET.
XX PA Dumas Milne Edwards J, Duclert A, Giordano J;
XX PI WPI; 2000-500381/45.
XX DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX PS Claim 1; SEQ ID 15277; 71pp + CD-ROM; English.
XX CC The present sequence is one of a large number of 5' ESTs derived from
XX CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX CC identified within the present sequence. The 5' ESTs were prepared from
XX CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX CC sequences usually correspond mainly to the 3' untranslated region (UTR)
XX CC of the mRNA because they are often obtained from oligo-dT primed cDNA
XX CC libraries. Such ESTs are not well suited for isolating cDNA sequences
XX CC derived from the 5' ends of mRNAs and even in those cases where longer
XX CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
XX CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
XX CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
XX CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX CC They are used to obtain upstream regulatory sequences and to design
XX CC expression and secretion vectors.
XX SQ Sequence 67 BP; 11 A; 21 C; 29 G; 6 T; 0 other;

Query Match 83.8%; Score 13.4; DB 21; Length 67;
Best Local Similarity 93.3%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgggagcgcgcgcg 15
   ||||| ||||| |||||
DB 29 cgggagcgcgcgcg 43

RESULT 10
AAT42053
ID AAT42053 standard; DNA; 25 BP.
XX AC AAT42053;
XX XX
XX 29-JAN-1997 (first entry)
XX DE Exotoxin A gene PCR primer.
XX XX
XX KM Exotoxin A; ETA; cytotoxin; Pseudomonas aeruginosa;
XX KM single chain antibody; scFv; monoclonal antibody; MAb; EGF;
XX KM epidermal growth factor; receptor; cancer; therapy; antitumour;
XX KM polymerase chain reaction; PCR; primer; ss.
XX OS Synthetic.
XX PN EP739984-A1.
XX PD 30-OCT-1996.
XX PF 26-APR-1995; 95EP-0106275.
XX PR 26-APR-1995; 95EP-0106275.
XX XX

```


CC in selected tissues. This sequence represents a PCR primer used in
CC the amplification of the murine DEDD protein described in the method of
CC the invention.

XX Sequence 35 BP; 6 A; 10 C; 16 G; 3 T; 0 other;

Query Match 80.0%; Score 12.8; DB 21; Length 35;
Best Local Similarity 87.5%; Pred. No. 7.7e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggagagcgcgcgagc 16
||||| |||||
DB 9 cggagagcgcgcgagc 24

RESULT 13
AAQ14201/c
ID AAQ14201 standard; DNA; 38 BP.

XX AAQ14201;

DT 10-JAN-1992 (first entry)

XX Probe P1672 for Giardia lamblia 18S rRNA.

KM Ribosomal RNA; diarrhoea; ss.

XX Synthetic.

OS EPA53290-A.

PN 23-OCT-1991.

PD 18-APR-1991; 91EP-0303479.

XX 18-APR-1990; 90US-0510476.

XX (GENE-) GENE-TRAK SYSTEM CORPORATION.

XX Shah JS, Buharin A, Lane DJ;

DR WPI, 1991-312505/43.

PT 18S ribosomal DNA or RNA nucleic acid probes - for the specific and
PT accurate detection of Giardia lamblia.

XX Claim 1; Fig 1; 32pp; English.

CC The probe hybridises to a region of the G. lamblia 18S rRNA which
CC starts at position corresponding to the region between bases
CC 500-409 of the E. coli sequence. It can be used for the detection
CC of this parasite which is a common cause of diarrhoea.
CC See also AAQ14197-Q14203.

XX Sequence 38 BP; 0 A; 16 C; 17 G; 5 T; 0 other;

Query Match 80.0%; Score 12.8; DB 12; Length 38;
Best Local Similarity 87.5%; Pred. No. 7.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggagagcgcgcgagc 16
||||| |||||
DB 36 CGCGAGCGAGCGCGGC 21

RESULT 14
AAK52519/c
ID AAK52519 standard; DNA; 47 BP.

XX AAK52519;
AC
XX

DT 25-JUN-1999 (first entry)

XX PCR primer for in situ analysis of DNA35918-1174.

XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy;
XX fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
XX anti-thrombotic; wound healing; tissue repair; PCR primer; ss.

XX Synthetic.

XX WO914328-A2.

XX 25-MAR-1999.

PF 16-SEP-1998; 98WC-US19330.

XX 25-NOV-1997; 97US-0066840.

XX 17-SEP-1997; 97US-0059113.

XX 17-SEP-1997; 97US-0059115.

XX 17-SEP-1997; 97US-0059117.

XX 17-SEP-1997; 97US-0059119.

XX 17-SEP-1997; 97US-0059121.

XX 17-SEP-1997; 97US-0059122.

XX 17-SEP-1997; 97US-0059184.

XX 18-SEP-1997; 97US-0059263.

XX 18-SEP-1997; 97US-0059266.

XX 15-OCT-1997; 97US-0062125.

XX 17-OCT-1997; 97US-0062285.

XX 21-OCT-1997; 97US-0063287.

XX 21-OCT-1997; 97US-0063486.

XX 24-OCT-1997; 97US-0062814.

XX 24-OCT-1997; 97US-0062816.

XX 24-OCT-1997; 97US-0063045.

XX 24-OCT-1997; 97US-0063120.

XX 24-OCT-1997; 97US-0063121.

XX 24-OCT-1997; 97US-0063127.

XX 24-OCT-1997; 97US-0063128.

XX 27-OCT-1997; 97US-0063329.

XX 27-OCT-1997; 97US-0063327.

XX 28-OCT-1997; 97US-0063541.

XX 28-OCT-1997; 97US-0063542.

XX 28-OCT-1997; 97US-0063544.

XX 28-OCT-1997; 97US-0063549.

XX 28-OCT-1997; 97US-0063550.

XX 29-OCT-1997; 97US-0063564.

XX 29-OCT-1997; 97US-0063435.

XX 29-OCT-1997; 97US-0063704.

XX 29-OCT-1997; 97US-0063732.

XX 29-OCT-1997; 97US-0063738.

XX 29-OCT-1997; 97US-0063734.

XX 29-OCT-1997; 97US-0064215.

XX 29-OCT-1997; 97US-0063735.

XX 31-OCT-1997; 97US-0063870.

XX 31-OCT-1997; 97US-0064103.

XX 03-NOV-1997; 97US-0064248.

XX 07-NOV-1997; 97US-0064809.

XX 12-NOV-1997; 97US-0065186.

XX 17-NOV-1997; 97US-0065846.

XX 18-NOV-1997; 97US-0065693.

XX 21-NOV-1997; 97US-0066120.

XX 21-NOV-1997; 97US-0066364.

XX 24-NOV-1997; 97US-0066772.

XX 24-NOV-1997; 97US-0066466.

XX 24-NOV-1997; 97US-0066770.

XX 24-NOV-1997; 97US-0066511.

XX 24-NOV-1997; 97US-0066453.

XX (GETH) GENENTECH INC.

PI Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;
 XX WPI; 1999-229533/19.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT gastrointestinal ulceration
 PS
 XX Example 74; Page 179; 320pp; English.
 CC Oligonucleotides AAX52276-532 represent PCR primers and probes used
 CC to isolate and amplify cDNA encoding secreted and transmembrane human
 CC proteins (see AAX52213-74 and AAX1344-403). The cDNA sequences are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides
 CC have specific uses based on their homology to known polypeptides,
 CC e.g. PRO211 and PRO217 can be used for disorders associated with the
 CC preservation and maintenance of gastrointestinal mucosa and the
 CC repair of acute and chronic mucosal lesions (e.g. enterocolitis,
 CC Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital
 CC microvillus atrophy), skin diseases associated with abnormal
 CC keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as
 CC lung squamous cell carcinoma of the vulva and gliomas), potent effects on
 CC cell growth and development, diseases related to growth or survival of
 CC nerve cells including Parkinson's disease, Alzheimer's disease, ALS,
 CC neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for
 CC reducing dermal scarring. PRO264 can be used as a target for anti-tumor
 CC drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia
 CC areata; PRO269 can be used as an anti-thrombotic agent; PRO287
 CC polypeptides and portions may have therapeutic applications in wound
 CC healing and tissue repair; PRO317 can be used for treating problems of
 CC the kidney, uterus, endometrium, blood vessels, or related tissue, e.g.
 CC in the heart of genital tract.
 XX
 SQ Sequence 47 BP; 8 A; 17 C; 10 G; 12 T; 0 other;

Query Match 80.0%; Score 12.8; DB 20; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggagcgcgcgcgcg 16
 | | | | | | | | | |
 Db 41 CAGGAGCGAGCGCGGC 26

RESULT 15
 AAF72719/c
 ID AAF72719 standard; DNA; 47 BP.
 XX
 XX AAF72719;
 AC
 XX
 XX
 DT 24-APR-2001 (first entry)
 XX
 XX
 DE Human PRO polypeptide gene oligonucleotide SEQ ID NO: 362.
 XX
 KW Human; PRO; dermatological; antiproliferative; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiac;
 KW antiangiogenic; vasotropic; antidiabetic; antineoplastic; cancer;
 KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischemia; inflammation; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 XX 22-FEB-2000; 2000WO-US04414.
 PF
 XX 07-JUL-1999; 99US-0143048.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.

PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-NOV-1999; 99WO-US23214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 05-JAN-2000; 99WO-US00219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N,
 PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A,
 PI Godowski PJ, Gimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ,
 PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D,
 PI Williams PM, Wood WI;
 DR WPI; 2001-081051/09.
 XX
 PT Sixty one nucleic acids encoding PRO polypeptides which are useful in
 PT the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung
 PT squamous cell carcinoma) and neurodegenerative diseases (e.g.
 PT Alzheimer's disease) -
 PS
 XX Example 102; Page 247; 393pp; English.

The present sequence is a probe which was used in the isolation of one
 CC of sixty one nucleic acids encoding novel secreted and transmembrane PRO
 CC polypeptides. The PRO polypeptides are useful for treating skin diseases
 CC (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
 CC gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
 CC diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
 CC cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
 CC ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
 CC disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
 CC infertility, AIDS and diabetes and retinal disorders such as retinitis
 CC pigmentosum. The PRO nucleic acids have applications in molecular
 CC biology, including use as hybridization probes, and in chromosome and
 CC gene mapping.

SQ Sequence 47 BP; 8 A; 17 C; 10 G; 12 T; 0 other;

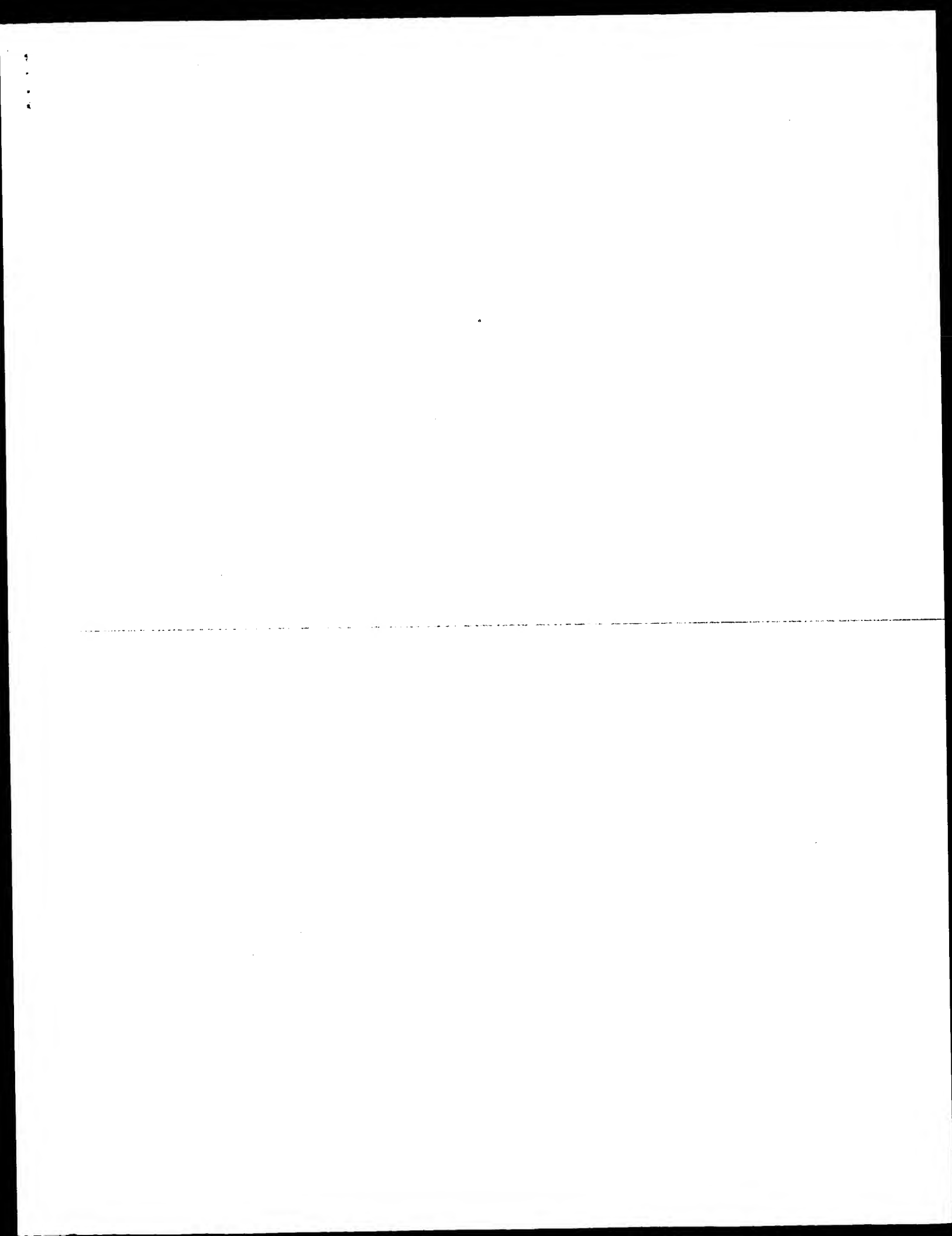
Query Match 80.0%; Score 12.8; DB 22; Length 47;
 Best Local Similarity 87.5%; Pred. No. 7.4e+03;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggagcgcgcgcgcg 16
 | | | | | | | | | |
 Db 41 CAGGAGCGAGCGCGGC 26

Search completed: June 28, 2002, 22:40:21
 Job time: 8097 sec

Mon Jul 1 08:40:51 2002

us-09-709-170a-16.szlm75.rng



US-08-465-485A-16

RESULT 4
US-08-123-936-374/C
Sequence 374, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
NUMBER OF SEQUENCES: 640
TITLE OF INVENTION: DNA-Binding Molecules
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (pcl-2) proto-oncogene
US-08-123-936-374

Query Match 100.0%; Score 16; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgagcgagc 16
|||||
DB 43 CGGAGCGCGCGCGGC 28

RESULT 5
US-08-475-228A-374/C
Sequence 374, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.

APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (pcl-2) proto-oncogene
US-08-475-228A-374

Query Match 100.0%; Score 16; DB 2; Length 50;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggagagcgagcgagc 16
|||||
DB 43 CGGAGCGCGCGCGGC 28

RESULT 6
US-08-482-080A-374/C
Sequence 374, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods

NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/111,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
US-08-482-080A-374

Query Match Best Local Similarity 100.0%; Score 16; DB 3; Length 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cggagcgcgcgcgcg 16
Db 43 CGGAGCGCGCGCGGC 28

RESULT 7
PCT-US93-12388-374/c
Sequence 374, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City

STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human B-cell leukemia/lymphoma 2
INDIVIDUAL ISOLATE: (bcl-2) proto-oncogene
PCT-US93-12388-374

Query Match Best Local Similarity 100.0%; Score 16; DB 5; Length 50;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 cggagcgcgcgcgcg 16
Db 43 CGGAGCGCGCGCGGC 28

RESULT 8
US-08-983-466-30/c
Sequence 30, Application US/08983466
Patent No. 6207372
GENERAL INFORMATION:
APPLICANT: SHUBER, ANTHONY P.
TITLE OF INVENTION: UNIVERSAL PRIMER SEQUENCE FOR MULTIPLEX
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAE-YENTER LAW GROUP
STREET: 260 Sheridan Ave., Ste. 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,466
FILING DATE: 10-FEB-1998
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,450
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W096/41012
FILING DATE: 06-JUNE-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rae-Venter, Barbara
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: GECO.001.01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 328-4400
TELEFAX: (650) 328-4477
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide primer"
US-08-983-466-30

Query Match 77.5%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgagcgagc 16
|||
Db 15 GGGGCGCGCGGCGC 2

RESULT 9
US-08-049-264C-28/C
Sequence 28, Application US/0804264C
Patent No. 5518901
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
TITLE OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,264C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1313.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-049-264C-28

Query Match 77.5%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgagcgagc 16
|||
Db 15 GGGGCGCGCGGCGC 2

RESULT 10
US-08-476-562-28/C
Sequence 28, Application US/08476562
Patent No. 5688669
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
TITLE OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,562
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/049,264
FILING DATE: April 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1313.004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-476-562-28

Query Match 77.5%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgagcgagc 16
|||
Db 15 GGGGCGCGCGGCGC 2

RESULT 11
US-08-479-723A-28/C
Sequence 28, Application US/08479723A
Patent No. 5744306
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.

TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
NUMBER OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
STREET: Peachtree Street N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,723A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 05010.0061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
TELEFAX: (404) 688-9880
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-08-479-723A-28

Query Match 77.5%; Score 12.4; DB 1; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgcgcgc 16
|||
Db 15 GGGGGCGCGCGCGC 2

RESULT 12
PCT-US94-04310-28/C
Sequence 28, Application PC/TUS9404310
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
NUMBER OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 74
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EFO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04310
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,264
FILING DATE: 19-APR-1993
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US94-04310-28

Query Match 77.5%; Score 12.4; DB 5; Length 21;
Best Local Similarity 92.9%; Pred. No. 3e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgcgcgc 16
|||
Db 15 GGGGGCGCGCGCGC 2

RESULT 13
US-09-677-045-10/C
Sequence 10, Application US/09677045
Patent No. 6346386
GENERAL INFORMATION:
APPLICANT: Elenitoba-Johnson, Koji
TITLE OF INVENTION: Method of Solution-based Scanning for Alterations in a
TITLE OF INVENTION: DNA Segment Using a Double-stranded DNA Binding Dye and
TITLE OF INVENTION: Fluorescence Melting Profiles
FILE REFERENCE: 2379.2.5
CURRENT APPLICATION NUMBER: US/09/677,045
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 40
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide
US-09-677-045-10

Query Match 77.5%; Score 12.4; DB 4; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.6e+03; 1; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ggaagcgcgcgcgcgc 16
|||
Db 15 GGGGGCGCGCGCGC 2

RESULT 14
US-08-049-264C-7/C
Sequence 7, Application US/08049264C
Patent No. 5518901
GENERAL INFORMATION:
APPLICANT: Murtagh, James J.
TITLE OF INVENTION: METHODS FOR NUCLEIC ACID DETECTION,
NUMBER OF INVENTION: SEQUENCING AND CLONING USING EXONUCLEASE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: Suite 1200, The Candler Bldg., 127
STREET: Peachtree Street N.E.
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,264C
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1313.001
TELECOMMUNICATION INFORMATION:

Mon Jul 1 08:40:51 2002

us-09-709-170a-16.szlm75.rml

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:51 ; Search time 334.55 Seconds
(without alignments)
11.013 Million cell updates/sec

Title: US-09-709-170A-15

Sequence: 15
1 cgcgcggcgacgca 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_NA: *
1: /cgn2_6/pdata/1/ina/5A.COMB.seq: *
2: /cgn2_6/pdata/1/ina/5B.COMB.seq: *
3: /cgn2_6/pdata/1/ina/6A.COMB.seq: *
4: /cgn2_6/pdata/1/ina/6B.COMB.seq: *
5: /cgn2_6/pdata/1/ina/PCRTUS.COMB.seq: *
6: /cgn2_6/pdata/1/ina/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-08-465-485A-15	Sequence 15, Appl
2	15	100.0	15	US-09-080-285-15	Sequence 15, Appl
3	13.4	89.3	69	US-08-343-443B-46	Sequence 46, Appl
4	12.4	82.7	17	5262866-3	Patent No. 5262866
5	11.8	78.7	18	US-08-519-300-2	Sequence 2, Appl
6	11.8	78.7	24	US-08-002-024B-11	Sequence 11, Appl
7	11.8	78.7	52	US-09-450-656-14	Sequence 14, Appl
8	11.4	76.0	30	US-09-150-900-32	Sequence 32, Appl
9	11.4	76.0	38	US-09-499-884-12	Sequence 12, Appl
10	11.4	76.0	41	PCT-US95-10973A-55	Sequence 55, Appl
11	11.4	76.0	45	US-08-171-389-300	Sequence 300, App
12	11.4	76.0	45	US-08-123-936-300	Sequence 300, App
13	11.4	76.0	45	US-08-475-228A-300	Sequence 300, App
14	11.4	76.0	45	US-08-482-080A-300	Sequence 300, App
15	11.4	76.0	45	PCT-US93-12388-300	Sequence 300, App
16	11.4	76.0	56	PCT-US95-10973A-56	Sequence 56, Appl
17	11.4	73.0	18	US-09-487-444-15	Sequence 15, Appl
18	10.8	72.0	18	US-08-739-401A-1	Sequence 1, Appl
19	10.8	72.0	18	US-08-602-264A-4	Sequence 4, Appl
20	10.8	72.0	18	US-08-602-264A-5	Sequence 5, Appl
21	10.8	72.0	18	US-09-205-860-9	Sequence 9, Appl
22	10.8	72.0	18	US-08-461-018A-4	Sequence 4, Appl
23	10.8	72.0	18	US-08-461-018A-5	Sequence 5, Appl
24	10.8	72.0	18	US-09-216-958-4	Sequence 4, Appl
25	10.8	72.0	18	US-09-216-958-5	Sequence 5, Appl
26	10.8	72.0	22	US-09-398-217-1	Sequence 1, Appl
27	10.8	72.0	22	US-09-562-331-1	Sequence 1, Appl

28	10.8	72.0	25	1	US-08-510-032A-5	Sequence 5, Appl
29	10.8	72.0	25	3	US-08-688-514-5	Sequence 5, Appl
30	10.8	72.0	27	3	US-09-126-280-6	Sequence 6, Appl
31	10.8	72.0	28	4	US-09-398-217-3	Sequence 3, Appl
32	10.8	72.0	28	4	US-09-562-331-3	Sequence 3, Appl
33	10.8	72.0	29	4	US-09-398-217-5	Sequence 5, Appl
34	10.8	72.0	29	4	US-09-398-217-7	Sequence 7, Appl
35	10.8	72.0	29	4	US-09-562-331-5	Sequence 5, Appl
36	10.8	72.0	29	4	US-09-562-331-7	Sequence 7, Appl
37	10.8	72.0	30	4	US-08-159-106-9	Sequence 9, Appl
38	10.8	72.0	30	6	US-08-159-106-9	Sequence 9, Appl
39	10.8	72.0	33	1	US-08-310-416A-8	Sequence 8, Appl
40	10.8	72.0	33	2	US-08-888-171-8	Sequence 8, Appl
41	10.8	72.0	33	3	US-08-840-316-106	Sequence 106, App
42	10.8	72.0	33	4	US-08-809-523-106	Sequence 106, App
43	10.8	72.0	34	4	US-08-471-971-106	Sequence 19, Appl
44	10.8	72.0	34	1	US-08-458-084-19	Sequence 19, Appl
45	10.8	72.0	34	1	US-08-205-508-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-08-465-485A-15
Sequence 15, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.O.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-15

Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGGCGGCGACGGA 15
DB 1 CGCGGCGGCGACGGA 15

RESULT 2
US-09-080-285-15
; Sequence 15, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-15

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGGCGGCGACGGA 15
DB 1 CGCGGCGGCGACGGA 15

RESULT 3
US-08-343-443B-46
; Sequence 46, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurtas, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmarte, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles
; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
; NUMBER OF SEQUENCES: 129
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 South Fifteenth Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: AEDIT 1.0 DOS text editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,443B
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00494
; FILING DATE: 19-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/06123
; FILING DATE: 20-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6121P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 69 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-343-443B-46

Query Match 89.3%; Score 13.4; DB 2; Length 69;
Best Local Similarity 93.3%; Pred. No. 4.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGCGGCGACGGA 15
DB 45 CGCGGCGGCGACGGA 59

RESULT 4
5262866-3/c
; Patent No. 5262866
; APPLICANT: FRITSCH, EDWARD F.; COLLINS, MARY
; TITLE OF INVENTION: PROCESS AND NUCLEIC ACID CONSTRUCT FOR

PRODUCING REAGENT COMPLEXES USEFUL IN DETERMINING TARGET
NUCLEOTIDE SEQUENCES
NUMBER OF SEQUENCES: 15
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/938,201
FILING DATE: 11-APR-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 729,504
FILING DATE: 02-MAY-1985
APPLICATION NUMBER: 607,885
FILING DATE: 07-MAY-1984
APPLICATION NUMBER: 684,308
FILING DATE: 20-DEC-1984
APPLICATION NUMBER: 684,305
FILING DATE: 20-DEC-1984
APPLICATION NUMBER: 607,885
FILING DATE: 07-MAY-1984
SEQ ID NO: 3:
LENGTH: 17
5262866-3

Query Match 82.7%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 1.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcggggcgacgga 15
||||| |||||||
Db 16 GCGCGGTCGACGGA 3

RESULT 5
US-08-519-300-2/C
Sequence 2, Application US/08519300
Patent No. 5834224
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Electrochemical Sensor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/519,300
FILING DATE: 8/23/96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 30 023.9
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: JOHN A. BAUER
REGISTRATION NUMBER: 32,554
REFERENCE/DOCKET NUMBER: HUBR-1070 PFF/JAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: oligonucleotide

US-08-519-300-2

Query Match 78.7%; Score 11.8; DB 2; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.8e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgcggggcgacgga 15
||||| |||||||
Db 17 GCGCGGTCGACGGA 3

RESULT 6
US-08-002-024B-11/C
Sequence 11, Application US/08002024B
Patent No. 5798103
GENERAL INFORMATION:
APPLICANT: MOOI, Frederik R
TITLE OF INVENTION: WHOPPING COUGH VACCINE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTRY: US
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,024B
FILING DATE: 08-JAN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92200038.5
FILING DATE: 08-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Robert J
REGISTRATION NUMBER: 17,355
REFERENCE/DOCKET NUMBER: BO-37424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703/521-2297
TELEFAX: 703/685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
US-08-002-024B-11

Query Match 78.7%; Score 11.8; DB 1; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgcggggcgacgga 15
||||| |||||||
Db 20 GCGCGGTCGACGGA 6

RESULT 7
US-09-450-656-14/C
Sequence 14, Application US/09450656
Patent No. 6251606
GENERAL INFORMATION:
APPLICANT: HSEU, Ruey-Shyang

APPLICANT: CHEN, Chh-Shang
TITLE OF INVENTION: Gene Sequence and Method for Distinguishing Cordyceps Sinensis
Patent No. 6251606
FILE REFERENCE: 2410-166P
CURRENT APPLICATION NUMBER: US/09/450,656
CURRENT FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 52
TYPE: DNA
ORGANISM: Cordyceps liangshanensis
US-09-450-656-14

Query Match 78.7%; Score 11.8; DB 4; Length 52;
Best Local Similarity 86.7%; Pred. No. 2.4e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgcgcggcgacgca 15
||||| |||
DB 29 CGCGCGCGCGCGGA 15

RESULT 8
US-09-150-900-32
Sequence 32, Application US/09150900
Patent No. 6207425
GENERAL INFORMATION:
APPLICANT: Liu, Qulang
APPLICANT: Sommer, Steve S.
TITLE OF INVENTION: BIDIRECTIONAL PCR AMPLIFICATION OF SPECIFIC ALLELES
FILE REFERENCE: BI-PASA
CURRENT APPLICATION NUMBER: US/09/150,900
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: 60/058575
EARLIER FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 32
LENGTH: 30
TYPE: DNA
ORGANISM: Homo sapiens
US-09-150-900-32

Query Match 76.0%; Score 11.4; DB 4; Length 30;
Best Local Similarity 92.3%; Pred. No. 3.9e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ggcgcggcgacgca 14
||||| |||
DB 3 ggcgcggcgacgca 15

RESULT 9
US-09-499-884-12
Sequence 12, Application US/09499884
Patent No. 6265172
GENERAL INFORMATION:
APPLICANT: St. Clair, Daret
APPLICANT: Urano, Muneyasu
APPLICANT: Kasarskis, Edward
TITLE OF INVENTION: DIAGNOSTIC TEST AND THERAPY FOR MANGANESE SUPEROXIDE DISMUTASE
FILE REFERENCE: 50229-180
CURRENT APPLICATION NUMBER: US/09/499,884
CURRENT FILING DATE: 2000-02-08
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 38
TYPE: DNA

ORGANISM: Homo sapiens
US-09-499-884-12

Query Match 76.0%; Score 11.4; DB 4; Length 38;
Best Local Similarity 92.3%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ggcgcggcgacgca 14
||||| |||
DB 26 ggcgcggcgacgca 38

RESULT 10
PCT-US95-10973A-55/C
Sequence 55, Application PC/TUS9510973A
GENERAL INFORMATION:
APPLICANT: Pflum Pharmaceuticals, Inc.
TITLE OF INVENTION: COMBUSTIBLES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGET
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10973A
FILING DATE: 29-AUG-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Notenburg, Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.413PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
PCT-US95-10973A-55

Query Match 76.0%; Score 11.4; DB 5; Length 41;
Best Local Similarity 92.3%; Pred. No. 3.7e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ggcgcggcgacgca 14
||||| |||
DB 27 ggcgcggcgacgca 15

RESULT 11
US-08-171-389-300
Sequence 300, Application US/08171389
Patent No. 5578444
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding

TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-171-389-300

Query Match 76.0%; Score 11.4; DB 1; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 3 gcggggcgacgga 15
|||||||
Db 31 GCGGGCGCCCGGA 43
RESULT 12
US-08-123-936-300
Sequence 300, Application US/08123936
Patent No. 5726014
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection of
TITLE OF INVENTION: DNA-Binding Molecules
NUMBER OF SEQUENCES: 640
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,936
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0075.32/G19P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-123-936-300

Query Match 76.0%; Score 11.4; DB 1; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 3 gcggggcgacgga 15
|||||||
Db 31 GCGGGCGCCCGGA 43
RESULT 13
US-08-475-228A-300
Sequence 300, Application US/08475228A
Patent No. 5869241
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: FTY, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475.228A
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-475-228A-300

Query Match 76.0%; Score 11.4; DB 2; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 gcggggcgacgga 15
|||||
Db 31 GCGGGGCGCCGGA 43

RESULT 14
US-08-482-080A-300
Sequence 300, Application US/08482080A
Patent No. 6010849
GENERAL INFORMATION:
APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
APPLICANT: Fry, Kirk E.
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 664
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,080A
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,389
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brady, John F.
REGISTRATION NUMBER: 39,118
REFERENCE/DOCKET NUMBER: 4600-0175.20/G19P3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
US-08-482-080A-300

Query Match 76.0%; Score 11.4; DB 3; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 gcggggcgacgga 15
|||||
Db 31 GCGGGGCGCCGGA 43

RESULT 15
PCT-US93-12388-300
Sequence 300, Application PC/TUS9312388
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12388
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783

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; FILING DATE: 23-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33,875
; REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human transferrin (Tf) gene
; PCT-US93-12388-300

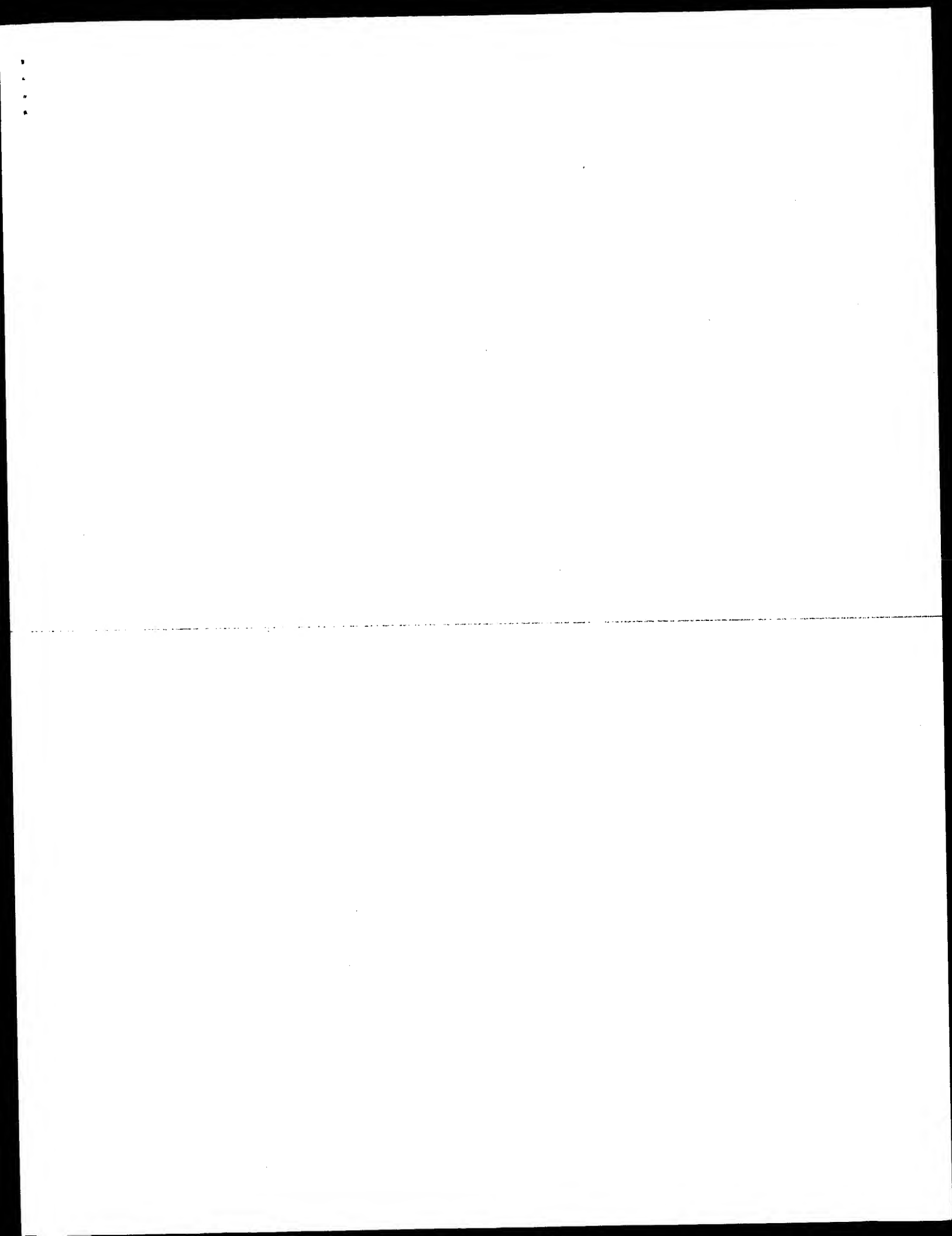
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Query Match          76.0%; Score 11.4; DB 5; Length 45;
Best Local Similarity 92.3%; Pred. No. 3.6e+03;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 3 gcggggcgagga 15
   | | | | | | | | |
Db 31 GCGGGGCGCCGGA 43

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Search completed: June 28, 2002, 22:16:52
 Job time: 8278 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:18 ; Search time 1381.16 Seconds
(without alignments)
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Title: US-09-709-170A-15

Sequence: 1 cggcgggcgagcagca 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	AA086657	Bcl-2 antisense ol
2	15	100.0	15	AAV28179	Antisense oligonuc
3	15	100.0	15	AAV23691	Deletion sequence
4	15	100.0	15	AAV18700	Target bcl-2 anti
5	12.4	82.7	29	AAV41907	Nucleotide sequence
6	12.4	82.7	71	AAV35957	5' primer used to
7	12.4	82.7	71	AAV35961	5' primer used to
8	11.8	78.7	24	AA048034	find primer #1. B
9	11.8	78.7	36	AAV52817	Oligonucleotide #1

C	10	11.8	78.7	36	19	AAV52818	Oligonucleotide #2
	11	11.8	78.7	40	21	AAV52327	Cenarchaena symbio
	12	11.8	78.7	40	21	AAV52998	Polynucleotide seq
C	13	11.8	78.7	50	22	AAV34175	Human SNP oligonuc
	14	11.8	78.7	51	22	AAH38708	Human SNP flanking
C	15	11.8	78.7	52	22	AAH38708	Cordyceps liangsha
C	16	11.8	78.7	74	21	AAH16720	Human secreted pro
C	17	11.4	76.0	18	24	AAH03344	S chrysomallus act
C	18	11.4	76.0	25	22	AAV90232	Genomic walking pr
	19	11.4	76.0	30	22	AAV30580	Human COMT gene PC
C	20	11.4	76.0	30	24	AAH03342	Streptomyces chrys
	21	11.4	76.0	38	22	AAH14353	Human manganese su
	22	11.4	76.0	40	22	AAH16088	Synthetic primer 4
	23	11.4	76.0	45	15	AAH69550	Human transferrin
	24	11.4	76.0	45	18	AAH64012	Human T-cell recep
	25	11.4	76.0	45	20	AAV17300	Test sequence from
C	26	11.4	76.0	47	21	AAH69475	Human map-related
	27	11.4	76.0	51	22	AAH3430	Human SNP oligonuc
C	28	11.4	76.0	51	22	AAH90447	Human clone cg4394
C	29	11.4	76.0	51	22	AAH90448	Human clone cg4394
C	30	11.4	76.0	59	18	AAH73794	Human FK-506 bindi
C	31	11.4	76.0	70	21	AAH20928	Human
C	32	11.4	76.0	70	21	AAH34806	Human adenosine re
C	33	11	73.3	17	23	ABR00033	Human NOGO Hammett
C	34	11	73.3	17	23	ABR00855	Human NOGO Inozyme
C	35	11	73.3	17	23	ABR00856	Human NOGO Inozyme
C	36	11	73.3	17	23	ABR01574	Human NOGO G-Cleav
C	37	11	73.3	17	23	ABR01817	Human NOGO Kinzyme
C	38	11	73.3	18	22	AAH26672	Human Smad7 phosph
C	39	11	73.3	23	11	AAH03769	Tissue plasminogen
C	40	11	73.3	29	21	AAH04042	Polymorphic fragme
C	41	11	73.3	30	14	AAH042711	Sequence of primer
C	42	11	73.3	46	24	AAH01544	Mycamineose biosynt
C	43	11	73.3	51	22	AAH27076	Human SNP oligonuc
C	44	11	73.3	60	22	AAH19843	Synthetic DNA for
C	45	10.8	72.0	15	22	AAH70023	Human TFRSFL1B ge

ALIGNMENTS

RESULT 1	AA086657	standard; DNA; 15 BP.
ID	AA086657	
XX	AA086657:	
XX		
XX	27-SEP-1995	(first entry)
DT		
XX		
XX	Bcl-2 antisense oligonucleotide.	
DE		
XX		
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;	
KW	Lymphoma; programmed cell death; ss.	
XX		
OS	Synthetic.	
XX		
XX	Key	Location/Qualifiers
FT	misc-feature	1..15
FT		/tag= "a
FT		/note= "3'-5' (antisense) sequence"
XX		
XX	W09508350-A.	
XX		
XX	30-MAR-1995.	
XX		
XX	20-SEP-1994;	94WO-US10725.
XX		
XX	20-SEP-1993;	93US-0124256.
XX		
XX	(REED/) REED J C.	
XX		
XX	Reed JC;	
XX		
XX		

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ8650-55) or the 5'-cap
CC region (AAQ8656-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 15 BP; 2 A; 4 C; 9 G; 0 T; 0 other;

Query Match 100.0%; Score 15; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcggggcgacgga 15
1 cggcggggcgacgga 15
Db 1 cggcggggcgacgga 15

RESULT 2
AAV28179
ID AAV28179 standard; DNA; 15 BP.
XX
AC AAV28179;
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KM Purification; oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
PI WPI; 1998-362922/31.
XX
DR WPI; 1998-362922/31.
XX
PT Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 84; 183pp; English.
XX
CC AAV2815-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 15 BP; 2 A; 4 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 15; DB 19; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcggggcgacgga 15
1 cggcggggcgacgga 15
Db 1 cggcggggcgacgga 15

RESULT 3
AAV23691
ID AAV23691 standard; DNA; 15 BP.
XX
AC AAV23691;
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 144.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
PI WPI; 1999-205198/17.
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 152; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 15 BP; 2 A; 4 C; 9 G; 0 U; 0 other;

Query Match 100.0%; Score 15; DB 20; Length 15;

KM	Screening; functional polypeptide; ligand; non-functional;
KW	enrichment; single chain antibody; PCR primer; ss.
XX	
OS	Synthetic.
PN	WO9920749-A1.
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98WO-GB03135.
PR	21-NOV-1997; 97US-0066729.
PR	20-OCT-1997; 97GB-0022131.
PR	13-NOV-1997; 97US-0065428.
XX	
PA	(MEDT-) MEDICAL RES COUNCIL.
XX	
PI	Tomlinson I, Winter G;
DR	WPI; 1999-288302/24.
XX	
PT	
XX	
PS	Example 2; Page 50; 67pp; English.
CC	The specification describes a method for screening for functional
CC	polypeptides which bind a ligand. The method comprises contacting a
CC	repertoire of polypeptides with a generic ligand' and then screening
CC	selected functional polypeptides with a target ligand. The method
CC	permits the removal from a chosen repertoire of the introduction of
CC	which are non-functional, e.g. as a result of the introduction of
CC	frame-shift mutations, stop codons, folding mutants or expression
CC	mutants which would be or are incapable of binding to any target
CC	ligand. The method also permits the enrichment of a chosen repertoire
CC	of polypeptides for those polypeptides which are functional, well folded
CC	and highly expressed. The polypeptides obtained can be used in
CC	diagnostic, prophylactic and therapeutic procedures. PCR primers
CC	AA33557-58 were used to amplify a germline V gene fragment, which was
CC	used in the construction of libraries of the invention.
XX	
SO	Sequence 71 BP; 12 A; 17 C; 33 G; 9 T; 0 other;
Query Match	82.7%; Score 12.4; DB 20; Length 71;
Best Local Similarity	92.9%; Pred. No. 5.7e+03;
Matches 13; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	2 ggcgggagcagca 15
Db	40 ggcgggtcgacgca 53
RESULT 7	
AA35961	
ID	AA35961 standard; DNA; 71 BP.
XX	
AC	AA35961.
XX	
DT	15-JUL-1999 (first entry)
XX	
DE	5' primer used to amplify germline V gene segment DPK9#.
XX	
KW	Screening; functional polypeptide; ligand; non-functional;
KW	enrichment; single chain antibody; PCR primer; ss.
XX	
OS	Synthetic.
XX	
PN	WO9920749-A1.
XX	
PD	29-APR-1999.
XX	
PF	20-OCT-1998; 98WO-GB03135.
XX	

PR 21-NOV-1997; 97US-0066729.
PR 20-OCT-1997; 97GB-0022131.
PR 13-NOV-1997; 97US-0065428.
PA
XX (MEDI-) MEDICAL RES COUNCIL.
PI Tomlinson I, Winter G;
XX
DR WPI: 1999-288302/24.
XX
XX Screening for functional polypeptides which bind a ligand
PS Example 2; page 50; 67pp; English.

The specification describes a method for screening for functional polypeptides which bind a ligand. The method comprises contacting a repertoire of polypeptides with a generic ligand¹ and then screening selected functional polypeptides with a target ligand. The method permits the removal from a chosen repertoire of polypeptides, those which are non-functional, e.g. as a result of the introduction of frame-shift mutations, stop codons, folding mutants or expression mutants which would be or are incapable of binding to any target ligand. The method also permits the enrichment of a chosen repertoire of polypeptides for those polypeptides which are functional, well folded and highly expressed. The polypeptides obtained can be used in diagnostic, prophylactic and therapeutic procedures. PCR primers AA33560-61 were used to amplify a gemline V gene fragment, which was used in the construction of libraries of the invention.

Sequence 71 BP; 12 A; 17 C; 33 G; 9 T; 0 other;

Query Match	82.7%	Score 12.4	DB 20	Length 71
Best Local Similarity	92.9%	Pred No. 5.7e+03		
Matches 13	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy	2	ggcgggcgacagga	15	
Db	40	ggcgggcgacagga	53	
RESULT 8				
ID	AA048034/c			
	AA048034 standard; DNA; 24 BP.			
XX	AA048034;			
XX	08-FEB-1994 (first entry)			
XX	finM primer #1.			
XX	N-terminal; minor; fimbrial subunit; B. pertussis; fimbriae; finM;			
KM	vacine; whooping cough; immune response; B. parapertussis; PCR;			
KW	B. bronchiseptica; polymerase chain reaction; primer; amplify; ss.			
XX	Bordetella pertussis.			
OS				
XX	EP555894-A.			
PN				
XX	18-AUG-1993.			
PD				
XX	08-JAN-1993; 93BP-0200047.			
PF				
XX	08-JAN-1992; 92EP-0200038.			
XX				
XX	(NEWE-) NEDERLANDEN MIN WEIZIJN.			
PA				
XX	Mooi FR;			
PI				
XX	WPI; 1993-260156/33.			
XX				
XX	Vaccines against whooping cough - contains functional component			
PT	of fimbriae of B. pertussis and can also be used in veterinary			

(2). The inventions can be used for the production of monoclonal antibodies for medical use which are of human type and therefore not antigenic in humans. They can also be used in the production of chimeric and transgenic animals which express useful foreign proteins, or which can serve as models for the study of human diseases. AAY52755 to AAY52828 are PCR primers used in examples from the present invention.

Sequence 36 BP; 5 A; 12 C; 13 G; 6 T; 0 other;

Query Match

Best Local Similarity 78.7%; Score 11.8; DB 19; Length 36;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggcggggagcagca 15
1 | | | | | | | | | |
DB 35 CCGCGGTCGACGCA 21

RESULT 11

AAA55227 standard; DNA; 40 BP.

AC AAA55227;

DT 30-AUG-2000 (first entry)

DE Cenarchaeum symbiosum promoter nucleotide sequence SRO ID NO:81.

XX Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology;

KW characterisation; archae; therapeutic; industrial; laboratory;

KM promoter; ds.

XX Cenarchaeum symbiosum.

PN WO000018909-A2.

PD 06-APR-2000.

PF 29-SEP-1999; 99WO-US22752.

PR 29-SEP-1998; 98US-0102294.

PA (DIVE-) DIVERSA CORP.

PI Swanson RV, Feldman RA, Schleper C;

DR MPI; 2000-293148/25.

PT New nucleic acids and proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum, useful in characterizing the physiology of these archae and in therapeutic, industrial or laboratory techniques.

XX Example 8; Page 201; 210pp; English.

CC AAA55186 to AAA55226 and AAY90913 to AAY90951 represent nucleic acids and proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum. The nucleic acids and proteins identified in the present invention are useful in characterizing the physiology of these archae and can be used in therapeutic, industrial or laboratory techniques. AAA55227 to AAA55260 represent promoter sequences from Cenarchaeum symbiosum. AAA55261 to AAA55269 represent PCR primers and probes used in examples from the present invention.

CC Sequence 40 BP; 8 A; 8 C; 15 G; 9 T; 0 other;

Query Match

Best Local Similarity 78.7%; Score 11.8; DB 21; Length 40;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggcggggagcagca 15

DB 24 cggcggggagcagca 38
| | | | | | | | | |

RESULT 12

AAZ95998 standard; DNA; 40 BP.

AC AAZ95998;

DT 10-APR-2000 (first entry)

DE Polynucleotide sequence including binding site for BamHI.

KW ligand binding; restriction enzyme; nucleic acid determination;

KM pharmaceutical; BamHI; ss.

XX Synthetic.

PN WO963077-A2.

PD 09-DEC-1999.

PF 04-JUN-1999; 99WO-US12516.

PR 04-JUN-1998; 98US-0087905.

PR 03-JUN-1999; 99US-0324672.

PA (TME-) TM TECHNOLOGIES INC.

PI Lane MJ, Benight AS, Faldasz BD;

DR MPI; 2000-116369/10.

PT Modulating polynucleotide ligand binding site affinity using

determination of the flanking duplex sequences -

XX Example 1; Page 41; 62pp; English.

CC The invention provides a method for determining the sequence of polynucleotide flanking regions that modulate ligand binding characteristics of an adjacent binding site. The method comprises: (i) providing a number of different duplex polynucleotides, each having the same polynucleotide ligand binding site and a randomly synthesised sequence flanking the binding site; (ii) exposing the duplex to a ligand selective for the binding site; (iii) isolating the duplex to a ligand do not bind the ligand, and (iv) determining the nucleotide composition of the flanking duplex sequence by sequencing the duplex sequence adjacent to the binding site. The invention is used to modulate the ligand-binding characteristics of any nucleotide sequence. The invention is less costly and more efficient than prior art techniques that moderate ligand binding using small molecule pharmaceuticals. Sequences AAZ95762-296170 represent polynucleotide sequences including the binding site for the restriction enzyme BamHI and used in the course of the invention.

CC Sequence 40 BP; 3 A; 10 C; 21 G; 6 T; 0 other;

Query Match

Best Local Similarity 78.7%; Score 11.8; DB 21; Length 40;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 cggcggggagcagca 15
1 | | | | | | | | | |
DB 22 cggcggtcgcgcgca 36

RESULT 13

AAL34175/C standard; DNA; 50 BP.

AC AAL34175;

XX 24-JAN-2002 (first entry)
DT
XX
DE Human SNP oligonucleotide #7383.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neutrophilic; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000MO-US35498.
XX
XX 28-DEC-1999; 99US-0173419.
XX 27-DEC-2000; 2000US-0173419.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach M;
PI
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acid encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -
XX
XX
XX Claim 1; Page 3511; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms.
XX
SQ Sequence 50 BP; 10 A; 15 C; 16 G; 9 T; 0 other;

Query Match 78.7%; Score 11.8; DB 22; Length 50;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcgaggcgacga 15
IIIIIIIIII
DB 39 CGCGGGGCTACGCA 25

RESULT 14
AAH38708/C
ID AAH38708 standard; DNA: 51 BP.
XX
AC AAH38708;
XX
DT 14-AUG-2001 (first entry)

XX Human SNP flanking oligonucleotide SEQ ID 1504.
DE
XX
XX Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNEP; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; ds.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
XX 26-APR-2001.
XX
XX 13-OCT-2000; 2000MO-US28436.
XX
XX 15-OCT-1999; 99US-0160096.
XX
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX
XX Plcoult-Newburg L, Pohl M;
PI
XX
DR WPI; 2001-290930/30.
XX
XX
XX New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample -
XX
XX
XX Claim 1; Page 57; 83pp; English.
XX
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
XX primer extension (SNEP) primers, and the sequences of regions flanking
XX sites of single nucleotide polymorphisms SNPs. The present invention
XX includes kits for determining the presence or absence of a SNP, using the
XX oligonucleotides of the invention. The PCR primers are used to amplify a
XX The oligonucleotides are useful for genotyping a nucleic acid sample by
XX performing a single-nucleotide primer extension reaction. The
XX oligonucleotides are useful for determining the presence, absence or
XX identity of a SNP and for genotyping nucleic acid samples, for e.g. to
XX assess by association analysis the genotype of an individual or group of
XX individuals, having a pathological phenotypic trait suspected of being
XX caused by one or more SNPs. Phenotypic traits include diseases e.g.
XX agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
XX dystrophy, familial hypercholesterolemia, polycystic kidney disease,
XX osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
XX traits also include symptoms of or susceptibility to multifactorial
XX disease of which a component is or may be genetic such as autoimmune
XX diseases, including, rheumatoid arthritis, multiple sclerosis,
XX inflammation, cancer, nervous system diseases and infection by pathogenic
XX microorganism. The method is also useful in forensic investigations and
XX paternity analysis. The present sequence represents a fragment of human
XX DNA flanking the site of a single nucleotide polymorphism.
XX
SQ Sequence 51 BP; 8 A; 25 C; 5 G; 13 T; 0 other;

Query Match 78.7%; Score 11.8; DB 22; Length 51;
Best Local Similarity 86.7%; Pred. No. 1.1e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcgaggcgacga 15
IIIIIIIIII
DB 20 CGCGGGGCGACGCA 6

RESULT 15
AAS08614/C
ID AAS08614 standard; DNA: 52 BP.
XX
AC AAS08614;

XX 26-SEP-2001 (first entry)
 DT Cordyceps liangshanensis 18s rRNA gene fragment #2.
 DE 18s rRNA; NS5/6; Chinese medicine; CC1014ab; ds.
 XX Cordyceps liangshanensis.
 OS US6251606-B1.
 XX 26-JUN-2001.
 PD 30-NOV-1999; 99US-0450656.
 XX 30-NOV-1999; 99US-0450656.
 PR 30-NOV-1999; 99US-0450656.
 XX (HSEU/) HSEU R.
 PA (LOSS/) LO S.
 PA (WANG/) WANG S.
 XX Hseu R, Chen C;
 PI WPI: 2001-431962/46.
 DR New gene sequences, particularly the 18S rRNA gene sequence of the
 XX Cordyceps sinensis between NS3/NS6 primer pair, useful as the index for
 PT distinguishing C. sinensis from other Cordyceps species
 XX Disclosure: Fig 5; 20pp: English.
 PS The sequence represents part of the C. liangshanensis 18s rRNA gene
 CC between primer pair NS5/6. This sequence is unique to isolate
 CC CC1014ab. The sequences of the invention are useful as an index for
 CC distinguishing C. sinensis from other Cordyceps species, particularly for
 CC use in chinese medicine and health supplements where only a genuine C.
 CC sinensis strain contains the active therapeutic agent.
 XX Sequence 52 Bp; 5 A; 16 C; 17 G; 14 T; 0 other;
 SQ

Query Match 78.7%; Score 11.8; DB 22; Length 52;
 Best Local Similarity 86.7%; Pred. No. 1.1e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcggggagcgga 15
 |||||
 Db 29 CGGCGGGCGCGCGGA 15

Search completed: June 28, 2002, 22:40:19
 Job time: 8095 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:10 ; Search time 1381.16 Seconds
(without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170A-7

Perfect score: 20

Sequence: 1 g9gaagatgcgcacgctg 20

Scoring table: IDENTITY_NUC

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 16	AA086649
2	20	100.0	20 19	AAV19651
3	20	100.0	20 19	AAV19657
4	20	100.0	20 22	AAV15276
5	20	100.0	20 22	AAV12300
6	20	100.0	20 22	AAV12301
7	20	100.0	20 22	AAV77808
8	20	100.0	20 22	AAV77809
9	20	100.0	22 14	AAQ49816

C	10	20	100.0	22	14	AAQ49817
C	11	20	100.0	35	16	AAQ86644
C	12	20	100.0	35	19	AAV19652
C	13	19	95.0	20	22	AAV19657
C	14	18	90.0	18	19	AAV11591
C	15	17.6	88.0	21	21	AAV15064
C	16	17	85.0	17	19	AAV19661
C	17	17	85.0	19	20	AAV06730
C	18	16	80.0	17	19	AAV19660
C	19	15.8	79.0	51	23	ABL00944
C	20	15	75.0	15	22	AAV15281
C	21	15	75.0	15	22	AAV15282
C	22	15	75.0	17	19	AAV19662
C	23	14	70.0	36	22	AAV45307
C	24	13.8	69.0	50	22	AAV84516
C	25	13.8	69.0	60	22	AAV84517
C	26	13.8	69.0	70	22	AAV84518
C	27	13.6	68.0	27	17	AAV18338
C	28	13.6	68.0	70	21	AAV14111
C	29	13.4	67.0	24	24	ABV86324
C	30	13.4	67.0	24	24	ABV86325
C	31	13.2	66.0	47	17	AAV28357
C	32	13.2	66.0	47	17	AAV28359
C	33	13.2	66.0	51	21	AAV28359
C	34	13.2	66.0	51	21	AAV28359
C	35	13.2	66.0	51	21	AAV28359
C	36	13.2	66.0	51	21	AAV28359
C	37	13.2	66.0	51	21	AAV28359
C	38	13.2	66.0	51	21	AAV28359
C	39	13.2	66.0	51	21	AAV28359
C	40	13	65.0	17	19	AAV19659
C	41	13	65.0	17	19	AAV19659
C	42	13	65.0	18	16	AAQ86659
C	43	13	65.0	18	19	AAV25245
C	44	13	65.0	18	19	AAV27719
C	45	13	65.0	18	19	AAV28181

ALIGNMENTS

RESULT	1
AAQ86649	AAQ86649 standard; DNA; 20 Bp.
ID	AAQ86649;
AC	AAQ86649;
XX	
DT	27-SEP-1995 (first entry)
XX	
DE	Bcl-2 translation initiation site region.
XX	
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW	Lymphoma; programmed cell death; ss.
XX	
OS	Synthetic.
XX	
PN	W09508350-A.
PD	30-MAR-1995.
XX	
PF	20-SEP-1994; 94WO-US10725.
XX	
PR	20-SEP-1993; 93US-0124256.
XX	
PA	(REED/) REED J C.
XX	
PI	Reed JC;
XX	
DR	WPI; 1995-139394/18.
XX	
PT	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
XX	of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108bp; English.
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS11846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA086650-55) or the 5'-cap
 CC region (AA086656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence
 CC (AA086649) was used as a control.
 CC
 SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggaagatgagcgacgctg 20
 ||||||||||||||||
 Db 1 ggaagatgagcgacgctg 20

RESULT 2
 AAV19651/c
 ID AAV19651 standard; DNA; 20 BP.
 XX
 AC AAV19651;
 XX
 DT 12-JUN-1998 (first entry)
 XX
 DE Human bcl-2 antisense oligonucleotide 1.
 XX
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5734033-A.
 XX
 PD 31-MAR-1998.
 XX
 PF 24-MAR-1994; 94US-0288692.
 XX
 PR 21-FEB-1992; 92US-0840716.
 PR 22-DEC-1988; 88US-0288692.
 PR 24-MAR-1994; 94US-0217082.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed J;
 XX
 DR WPI; 1998-229881/20.
 XX
 PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX
 PS Claim 6; Columns 3-4; 21pp; English.
 XX
 CC This antisense oligonucleotide is complementary to the translation
 CC initiation site of the human bcl-2 mRNA. The bcl-2 antisense
 CC oligonucleotides are phosphorothioate derivatives and can straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of
 CC a functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 CC
 SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 ggaagatgagcgacgctg 20
 ||||||||||||||||
 Db 20 GGGAAGATGGCGACGCTG 1

RESULT 3
 AAV19657
 ID AAV19657 standard; DNA; 20 BP.
 XX
 AC AAV19657;
 XX
 DT 12-JUN-1998 (first entry)
 XX
 DE Human bcl-2 transcription initiation sense (TI-S) oligonucleotide.
 XX
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5734033-A.
 XX
 PD 31-MAR-1998.
 XX
 PF 24-MAR-1994; 94US-0288692.
 XX
 PR 21-FEB-1992; 92US-0840716.
 PR 22-DEC-1988; 88US-0288692.
 PR 24-MAR-1994; 94US-0217082.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed J;
 XX
 DR WPI; 1998-229881/20.
 XX
 PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX
 PS Disclosure; Column 19; 21pp; English.
 XX
 CC This oligonucleotide is used as a control in measuring DNA fragmentation
 CC as an indicator of bcl-2 antisense oligonucleotide mediated programmed
 CC cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
 CC straddle strategic sites such as the translation initiation site, donor
 CC and acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 CC
 SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggaagatgagcgacgctg 20
 ||||||||||||||||
 Db 1 ggaagatgagcgacgctg 20

RESULT 4
 AAD15276/c
 ID AAD15276 standard; DNA; 20 BP.
 XX
 AC AAD15276;
 XX
 DT 15-NOV-2001 (first entry)

FT	/note="Optionally labelled with FITC
FT	(Fluoresceinisothiocyanate)"
FT	1..20
FT	/*tag" b
FT	/mod_base= OTHER
FT	/note= "Sulphate-Oligodeoxynucleotide"
XX	
PN	WO200159156-A2.
XX	
PD	16-AUG-2001.
XX	
PF	09-FEB-2001; 2001WO-IL00134.
XX	
PR	10-FEB-2000; 2000US-0181693.
XX	
PA	(YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX	
PI	Barenholz Y, Hirsch-lerner D, Cohen R, Dagan A, Gatt S;
XX	
DR	WPI; 2001-497084/54.
XX	
PT	Determining binding of compounds to a surface, particularly of DNA to
PT	transfection vesicle, using lipid-coupled fluorophore as pH- or
PT	potential-sensitive probe -
XX	
PS	Example 4; Page 20; 39pp; English.
XX	
CC	The invention relates to a method for determining the binding of a
CC	species at a surface, where binding alters the local pH or the surface
CC	potential, by stable incorporation of a probe at the surface. Probe
CC	consists of a pH- or potential-sensitive fluorophore attached to either
CC	a steroid or a lipid having at least two alkyl or alkenyl chains of at
CC	least 14 carbons. A change in fluorescence from fluorophore when a
CC	species binds to, or is released from, the surface is detected.
CC	The method is used for determining the extent of binding of species,
CC	particularly a biomolecule (nucleic acid or protein) to a surface or its
CC	release from the surface. Particularly the surface is a lipid vesicle
CC	being used for DNA transfection or a cell membrane. The method is also
CC	useful for monitoring transfection of DNA to cells, in vivo or in vitro.
CC	The method is used for detecting both specific and non-specific
CC	interactions at the surface. The lipid/steroid component ensures stable
CC	incorporation of the probe, thus stable and reproducible observation of
CC	interactions. The present DNA sequence is an AM-TIS sulphate-
CC	oligodeoxynucleotide which is used to detect the binding of charged
CC	species.
XX	
SO	Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;
XX	
Query Match	100.0%; Score 20; DB 22; Length 20;
Best Local Similarity	100.0%; Pred. No. 1.5;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 gggaagatggcgacgctg 20
Db	1 gggaagatggcgacgctg 20
RESULT 6.	
ADAD12301/C	
ADAD12301 standard; DNA; 20 BP.	
AC	ADAD12301;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Bcl2-TIAS sulphate-oligonucleotide to detect binding of charged species.
XX	
DE	Bcl2-TIAS sulphate-oligonucleotide; DNA transfection; fluorophore;
KM	biomolecule; charged species; lipid vesicle; ss.
XX	
OS	unidentified.
XX	

DR WPI: 2001-257588/26.
XX
XX Delivering antisense oligodeoxynucleotide to cells for treating
PT cancers, involves forming a complex comprising the oligodeoxynucleotide
PT and a polynuclear platinum compound, and providing the complex to the
PT cells
XX
PS Example 4; Page 28; 52pp; English.
XX
CC The present invention relates to a method for delivering an antisense
CC oligodeoxynucleotide to cells. The method comprises forming a complex
CC comprising the antisense oligonucleotide and a polynuclear platinum
CC compound, and providing the complex to the cells. The present sequence is
CC a control sense oligonucleotide which was used in an assay for Bcl-2
CC antisense oligonucleotide activity (see AAF77808). Bcl-2 is a suppressor
CC of apoptosis and its expression in cancer cells may contribute to the
CC resistance of cancer cells to apoptosis. The complex of the present
CC invention is useful for treating cancer and any other disease amenable to
CC the treatment by antisense oligonucleotides.
CC
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcgcacgctg 20
DB 1 gggaagatgagcgcacgctg 20
|||||

RESULT 9
AAQ49816/c
ID AAQ49816 standard; DNA; 22 BP.
XX
XX AAQ49816;
AC
XX
XX 03-MAY-1994 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
XX Synthetic.
OS
XX
XX WO9320200-A.
PN
XX
XX 14-OCT-1993.
PD
XX
XX 02-APR-1993; 93WO-GB00686.
PE
XX
XX 02-APR-1992; 92GB-0007275.
PR
XX 02-APR-1992; 92GB-0007276.
PS
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Evan GI;
PI
XX
XX WPI: 1993-336908/42.
DR
XX
XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing Bcl-2
XX
XX
PS Disclosure; Page 58; 109pp; English.
XX
XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.

CC of bcl-2 antisense oligonucleotides.
XX
SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcgcacgctg 20
DB 22 GGGAAGATGAGCGCACGCTG 3
|||||

RESULT 10
AAQ49817/c
ID AAQ49817 standard; RNA; 22 BP.
XX
XX AAQ49817;
AC
XX
XX 03-MAY-1994 (first entry)
DT
XX
XX Bcl-2 antisense oligonucleotide.
DE
XX
XX Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
XX Synthetic.
OS
XX
XX WO9320200-A.
PN
XX
XX 14-OCT-1993.
PD
XX
XX 02-APR-1993; 93WO-GB00686.
PE
XX
XX 02-APR-1992; 92GB-0007275.
PR
XX 02-APR-1992; 92GB-0007276.
PS
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Evan GI;
PI
XX
XX WPI: 1993-336908/42.
DR
XX
XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing Bcl-2
XX
XX
PS Disclosure; Page 58; 109pp; English.
XX
XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC of bcl-2 antisense oligonucleotides.
XX
XX
SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 U; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcgcacgctg 20
DB 22 GGGAAGATGAGCGCACGCTG 3
|||||

RESULT 11
AAQ86644
ID AAQ86644 standard; DNA; 35 BP.
XX

AC AA086644;
 XX
 DT 27-SEP-1995 (first entry)
 XX
 DE Bcl-2 translation initiation region.
 XX
 KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW Leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN W09508350-A.
 XX
 PD 30-MAR-1995.
 XX
 PF 20-SEP-1994; 94WO-US10725.
 XX
 PR 20-SEP-1993; 93US-0124256.
 XX
 PA (REED/) REED J C.
 XX
 PI Reed JC;
 XX
 DR WPI; 1995-139394/18.
 XX
 PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Disclosure; Page 13; 108pp; English.
 XX
 CC The antisense oligonucleotide TI-AS (AA086643) straddles the
 CC translation-initiation site in the mRNA coding strand of the human
 CC bcl-2 gene and is complementary to this region. It reduces the
 CC expression of bcl-2 gene product thereby inducing programmed cell
 CC death of certain cancer cells. The corresp. sense bcl-1 sequence
 CC was synthesized for use as a control.
 XX
 SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;
 XX

Query Match 100.0%; Score 20; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatgagcgacgctg 20
 |||||
 Db 11 ggggaagatgagcgacgctg 30

RESULT 12
 AAV19652
 ID AAV19652 standard; DNA; 35 BP.
 XX
 AC AAV19652;
 XX
 DT 12-JUN-1998 (first entry)
 XX
 DE Human bcl-2 oligonucleotide 1.
 XX
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukemia; human;
 KW cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5734033-A.
 XX
 PD 31-MAR-1998.
 XX
 PF 24-MAR-1994; 94US-0288692.
 XX
 PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.
 PR 24-MAR-1994; 94US-0217082.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed J;
 XX
 DR WPI; 1998-229881/20.
 XX
 PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX
 PS Claim 1; Columns 3-4; 21pp; English.
 XX
 CC This is a human bcl-2 oligonucleotide based on which an antisense
 CC oligonucleotide complementary to the translation initiation site of the
 CC human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
 CC straddle strategic sites such as the translation initiation site, donor
 CC and acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 XX
 SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;
 XX

Query Match 100.0%; Score 20; DB 19; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatgagcgacgctg 20
 |||||
 Db 11 ggggaagatgagcgacgctg 30

RESULT 13
 AAC86407/c
 ID AAC86407 standard; RNA; 20 BP.
 XX
 AC AAC86407;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Human bcl-xl and bcl-2 mRNA antisense control sequence CO2.
 XX
 KW Human; bcl-xl; bcl-2; apoptosis; antisense; cancer; allergic disease;
 KW restenosis; fibrosis; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN W020006724-A2.
 XX
 PD 09-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-EP03708.
 XX
 PR 30-APR-1999; 99GB-0010119.
 XX
 PA (UYZU-) UNIV ZUERICH.
 XX
 PI Zangemeister-Wittke U, Luedke G, Huesken D;
 XX
 DR WPI; 2001-015981/02.
 XX
 PT Antisense oligonucleotide derivatives directed against human bcl-xl
 PT mRNA and capable of modulating biosynthesis of human bcl-xl proteins,
 PT useful in treatment and diagnosis of hyperproliferative diseases -
 XX
 PS Example 2; Page 23; 38pp; English.
 XX
 CC The present invention provides antisense nucleotides which hybridise to
 CC the human bcl-xl and bcl-2 mRNA sequences. The bcl-xl and bcl-2 proteins

CC are involved in apoptosis, and the antisense strands can be used to
CC inhibit them and possibly lead to cell death. The nucleic acids of the
CC invention can be used in the treatment of cancer, particularly
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
CC types of allergic disease.

SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 95.0%; Score 19; DB 22; Length 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ggaagatgagcagcagctg 20
DB 20 GGAAGATGCGCAGCGTG 2

RESULT 14

AAV1591/c
ID AAV1591 standard; DNA; 18 BP.

XX AAV1591;

DT 30-JUL-1998 (first entry)

DE Liposomal bcl-2 antisense polynucleotide.

XX Bcl-2; antisense; disease; treatment; cancer; follicular lymphoma;
KW leukaemia; plasma cell dyscrasia; breast; prostate; colon;
XX autoimmune diseases; ss.

OS Synthetic.

OS Homo sapiens.

PN WC9814172-A1.

PD 09-APR-1998.

PF 03-OCT-1997; 97WO-US18348.

PR 04-OCT-1996; 96US-0726211.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Lopez-Berestein G, McDonnell TJ, Tara AM, Tormo M;

DR WPI; 1998-239841/21.

PT Composition comprising oligo:nucleotide anti-sense to Bcl-2 gene -
PT useful for, e.g. treatment of Bcl-2 related disease such as
PT follicular lymphoma and auto-immune disease

PS Claim 4; Page 30; 69pp; English.

CC This sequence is a nuclease-resistant p-ethoxy antisense oligonucleotide
CC which specifically binds to the translation initiation site of human
CC Bcl-2 mRNA. This oligonucleotide can be used in a method to treat Bcl-2
CC related disease in humans and animals, e.g. cancer especially follicular
CC lymphoma (FL), leukaemia, plasma cell dyscrasia, cancer of breast,
CC prostate and colon, or autoimmune diseases.

SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 90.0%; Score 18; DB 19; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 gaagatgagcagcagctg 20
DB 18 GAAGATGCGCAGCGTG 1

RESULT 15
AAC65064/c
ID AAC65064 standard; DNA; 21 BP.

XX AAC65064;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #8.

XX Antisense oligonucleotide; RNA molecule cleavage; immune activation;
KW bcl; protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

PN WC200061810-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09293.

PR 08-APR-1999; 99US-0128377.

PA (OAST-) OASIS BIOSCIENCES INC.

PI Brown BD, Riley TA;

DR WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal
PT bases, and modified backbone linkages is useful to target therapeutic
PT genes, preferably anti-apoptosis or chemoresistance genes

XX Example 7; Fig 3; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides
CC containing a number of degenerate bases and with a modified backbone
CC which can be used to direct cleavage of target RNA molecules. The use of
CC degenerate bases reduces the risk of immune activation following
CC injection into animals, which causes deleterious side effects associated
CC with many therapeutic antisense oligonucleotides. Sequences
CC AAC65029-C65077 are antisense oligonucleotides and PCR primers used in
CC assays to demonstrate the effects of the sequences of the invention.

SQ Sequence 21 BP; 2 A; 9 C; 4 G; 4 T; 2 other;

Query Match

Best Local Similarity 88.0%; Score 17.6; DB 21; Length 21;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 ggaagatgagcagcagctg 20
DB 21 GGAARNATGCGCAGCGTG 3

Search completed: June 28, 2002, 22:40:10
Job time: 8086 sec

Mon Jul 1 08:40:58 2002

us-09-709-170a-7.szlm75.rng

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 19:51:49 ; Search time 3762.88 Seconds
(without alignments)
111.226 Million cell updates/sec

Title: US-09-709-170A-1
Perfect score: 20
Sequence: 1 cagcgtgcgcacccctcc 20

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb.ba:*
2: gb.htg:*
3: gb.in:*
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5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sy:*
12: gb.un:*
13: gb.vl:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
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24: em.ph:*
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26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vl:*
30: em.htg.hum:*
31: em.htg.inv:*
32: em.htg.other:*
33: em.htg.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
------------	-------------	-------	--------	-------	-------------

1	20	100.0	20	6	AR052603	AR052603 Sequence
2	20	100.0	20	6	AR052609	AR052609 Sequence
3	20	100.0	20	6	AR176022	AR176022 Sequence
4	20	100.0	20	6	AR176023	AR176023 Sequence
5	20	100.0	20	6	AR211659	AR211659 Sequence
6	20	100.0	20	6	AX211670	AX211670 Sequence
7	20	100.0	20	6	AX277461	AX277461 Sequence
8	20	100.0	20	6	AX277461	AX277461 Sequence
9	20	100.0	20	6	196082	196082 Sequence 1
10	20	100.0	20	6	196088	196088 Sequence 7
11	20	100.0	22	6	A76123	A76123 Sequence 3
12	20	100.0	22	6	A76124	A76124 Sequence 4
13	20	100.0	35	6	AR052604	AR052604 Sequence
14	20	100.0	35	6	196083	196083 Sequence 2
15	19	95.0	20	6	AX045387	AX045387 Sequence
16	18	90.0	18	6	BD008994	BD008994 Inhibitio
17	17	85.0	17	6	196092	196092 Sequence 11
18	16	80.0	17	6	196091	196091 Sequence 10
19	15.8	79.0	29	5	AX165740	AX165740 Sequence
20	15.4	77.0	29	5	CHRC2A101	K02260 Chicken alp
21	15	75.0	15	6	AX277468	AX277468 Sequence
22	15	75.0	15	6	AX277469	AX277469 Sequence
23	14	70.0	17	6	196093	196093 Sequence 12
24	13.8	69.0	19	6	AX083694	AX083694 Sequence
25	13.8	69.0	50	6	AX133707	AX133707 Sequence
26	13.8	69.0	60	6	AX133708	AX133708 Sequence
27	13.6	68.0	70	6	AX133709	AX133709 Sequence
28	13.6	68.0	27	6	AR004426	AR004426 Sequence
29	13.6	68.0	27	6	143661	143661 Sequence 13
30	13.4	68.0	24	6	186720	186720 Sequence 8
31	13.2	66.0	27	6	AX290202	AX290202 Sequence
32	13.2	66.0	47	6	AR153764	AR153764 Sequence
33	13.2	66.0	51	6	AX157777	AX157777 Sequence
34	13.2	66.0	51	6	AX157778	AX157778 Sequence
35	13.2	66.0	51	6	AX157779	AX157779 Sequence
36	13	65.0	16	6	AX103898	AX103898 Sequence
37	13	65.0	16	6	AX355505	AX355505 Sequence
38	13	65.0	17	6	196090	196090 Sequence 9
39	13	65.0	18	6	AR052619	AR052619 Sequence
40	13	65.0	18	6	AR052624	AR052624 Sequence
41	13	65.0	18	6	AR116926	AR116926 Sequence
42	13	65.0	18	6	AR140496	AR140496 Sequence
43	13	65.0	18	6	AR146347	AR146347 Sequence
44	13	65.0	18	6	AR146392	AR146392 Sequence
45	13	65.0	18	6	AR154716	AR154716 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR052603 20 bp DNA
DEFINITION Sequence 1 from patent US 5831066.
ACCESSION AR052603
VERSION AR052603.1 GI:5975967
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A1 03-NOV-1998;
FEATURES
Location/Qualifiers
source
BASE COUNT 2 a 10 c 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best local Similarity 100.0%; Pred. No. 50;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 1 CAGCGTGCGCCATCCTTCCC 20

RESULT 2
AR052609/c AR052609 20 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 7 from patent US 5831066.
ACCESSION AR052609
VERSION AR052609.1 GI:5975973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 20 CAGCGTGCGCCATCCTTCCC 1

RESULT 3
AR176022 AR176022 20 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 1 from patent US 6310047.
ACCESSION AR176022
VERSION AR176022.1 GI:17917321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell, N. and Kloster, M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 1 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
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Db 1 CAGCGTGCGCCATCCTTCCC 20

RESULT 4
AR176023/c AR176023 20 bp DNA linear PAT 17-DEC-2001
LOCUS
DEFINITION Sequence 2 from patent US 6310047.
ACCESSION AR176023

VERSION AR176023.1 GI:17917322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell, N. and Kloster, M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 2 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 20 CAGCGTGCGCCATCCTTCCC 1

RESULT 5
AX211669/c AX211669 20 bp DNA linear PAT 06-SEP-2001
LOCUS
DEFINITION Sequence 1 from Patent WO0159156.
ACCESSION AX211669
VERSION AX211669.1 GI:15523901
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz, Y., Hirsch-Lerner, D., Cohen, R., Dagan, A. and Gatl, S.
TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 1 16-AUG-2001;
Yissum Research Development Co., the Hebrew University of Jerusalem (IL)

FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="."

BASE COUNT 4 a 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 20 CAGCGTGCGCCATCCTTCCC 1

RESULT 6
AX211670 AX211670 20 bp DNA linear PAT 06-SEP-2001
LOCUS
DEFINITION Sequence 2 from Patent WO0159156.
ACCESSION AX211670
VERSION AX211670.1 GI:15523902
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz, Y., Hirsch-Lerner, D., Cohen, R., Dagan, A. and Gatl, S.

TITLE Detection of binding of charged species using ph- or
potential-sensitive probes
JOURNAL Patent: WO 0159156-A 2 16-AUG-2001;
Yissum Research Development Co., The Hebrew University of Jerusalem
(IL)

FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
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Db 1 CAGCGTGGCCATCTTCCC 20

RESULT 7
AX277461 20 bp DNA PAT 29-OCT-2001
LOCUS AX277461
DEFINITION Sequence 1 from Patent WO0160998.
ACCESSION AX277461
VERSION AX277461.1 GI:16548979
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (sites)
AUTHORS Tari, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
TITLE Small oligonucleotides with anti-tumor activity
JOURNAL Patent: WO 0160998-A 1 23-AUG-2001;
Board of Regents, The University of Texas System (US)

FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Primer"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
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Db 1 CAGCGTGGCCATCTTCCC 20

RESULT 8
196082 20 bp DNA PAT 01-DEC-1998
LOCUS 196082
DEFINITION Sequence 1 from patent US 5734033.
ACCESSION 196082
VERSION 196082.1 GI:3940552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 1 31-MAR-1998;
Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
|||||
Db 1 CAGCGTGGCCATCTTCCC 20

RESULT 9
196088/c 20 bp DNA PAT 01-DEC-1998
LOCUS 196088
DEFINITION Sequence 7 from patent US 5734033.
ACCESSION 196088
VERSION 196088.1 GI:3940558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 7 31-MAR-1998;
Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
|||||
Db 20 CAGCGTGGCCATCTTCCC 1

RESULT 10
A76123 22 bp DNA PAT 19-OCT-1999
LOCUS A76123
DEFINITION Sequence 3 from Patent WO9320200.
ACCESSION A76123
VERSION A76123.1 GI:6088259
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 3 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
Location/Qualifiers
1..22
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcccattcttccc 20
|||||
Db 3 CAGCGTGGCCATCTTCCC 22

RESULT 11
LOCUS A76124 22 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 4 from Patent WO9320200.
ACCESSION A76124
VERSION A76124.1 GI:5088260
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan,G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 4 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
FEATURES
SOURCE 1..22
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacatcctccc 20
|||||
Db 3 CAGCGTGGCCATCCTTCCC 22

RESULT 12
LOCUS AR052604 35 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5831066.
ACCESSION AR052604
VERSION AR052604.1 GI:5975968
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 2 03-NOV-1998;
FEATURES
SOURCE 1..35
/organism="unknown"
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacatcctccc 20
|||||
Db 30 CAGCGTGGCCATCCTTCCC 11

RESULT 13
LOCUS 196083 35 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 2 from patent US 5734033.
ACCESSION 196083
VERSION 196083.1 GI:3940553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
FEATURES
SOURCE 1..35
/organism="unknown"
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacatcctccc 20
|||||
Db 30 CAGCGTGGCCATCCTTCCC 11

RESULT 14
LOCUS AX045387 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 7 from Patent WO0066724.
ACCESSION AX045387
VERSION AX045387.1 GI:11343871
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zangemeister-Wilke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mna
JOURNAL Patent: WO 0066724-A 7 09-NOV-2000;
FEATURES
SOURCE 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense"
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 15e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacatcctccc 19
|||||
Db 2 CAGCGTGGCCATCCTTCCC 20

RESULT 15
LOCUS BD008994 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Inhibition of Bcl-2 protein expression by liposomal antisense oligodeoxynucleotides.
ACCESSION BD008994
VERSION BD008994.1 GI:18637367
KEYWORDS JP 2001502172-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Torno,M., Tara,A.M., Berestrein,G.L. and McDonnell,T.J.
TITLE Inhibition of Bcl-2 protein expression by liposomal antisense oligodeoxynucleotides
JOURNAL Patent: JP 2001502172-A 1 20-FEB-2001;
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
OS Unidentified

PN JP 2001502172-A/1
 PD 20-FEB-2001
 PF 03-OCT-1997 JP 1998516985
 PR 04-OCT-1996 US 08/726211
 PI MAR TORMO, ANA M TARA, GABRIEL LOPEZ BERESTEIN, PI TIMOTHY J
 MCDONNELL
 PC A61K9/127, A61K31/70, C07H21/04, C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 PH key Location/Qualifiers
 FT source 1.18
 FT Location/Qualifiers
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 /db_xref="taxon:32644"
 BASE COUNT 2 a 8 c 4 g 4 t
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 cagcgtgcgcacaccc 18
 ||||||||||||
 Db 1 CAGCGTGCACCATCTTC 18

Search completed: June 28, 2002, 22:10:44
 Job time: 8335 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 20:25:24 ; Search time 1381.16 Seconds

(Without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170A-1

Perfect score: 20

Sequence: 1 cagcgtgcgcacatcctcc 20

Scoring table: IDENTITY_NTC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	16	AAQ86649
2	20	100.0	20	19	AAV19651
3	20	100.0	20	19	AAV19657
4	20	100.0	20	22	AAV15276
5	20	100.0	20	22	AAV12300
6	20	100.0	20	22	AAV12301
7	20	100.0	20	22	AAV17808
8	20	100.0	20	22	AAV17809
9	20	100.0	22	14	AAQ49816

10	20	100.0	22	14	AAQ49817
11	20	100.0	35	16	AAQ86644
12	20	100.0	35	19	AAV19652
13	19	95.0	20	22	AAQ86407
14	18	90.0	18	19	AAV11591
15	17.6	88.0	21	21	AAQ65064
16	17	85.0	17	19	AAV19661
17	17	85.0	19	20	AAQ6730
18	16	80.0	17	19	AAV19660
19	15.8	79.0	51	23	ABL00944
20	15	75.0	15	22	AAV15281
21	15	75.0	15	22	AAV15282
22	15	75.0	17	19	AAV19662
23	14	70.0	36	22	AAH45307
24	13.8	69.0	50	22	AAV84516
25	13.8	69.0	60	22	AAV84517
26	13.8	69.0	70	22	AAV84518
27	13.6	68.0	27	17	AAV18388
28	13.6	68.0	70	21	AAV18388
29	13.4	67.0	24	24	AAV18388
30	13.4	67.0	24	24	AAV18388
31	13.2	66.0	47	17	AAV28357
32	13.2	66.0	47	17	AAV28359
33	13.2	66.0	51	21	AAV6662
34	13.2	66.0	51	21	AAV6663
35	13.2	66.0	51	21	AAV6664
36	13.2	66.0	51	21	AAV6665
37	13.2	66.0	51	22	AAV74164
38	13.2	66.0	51	22	AAV74165
39	13.2	66.0	51	22	AAV74165
40	13	65.0	16	22	AAV98965
41	13	65.0	17	19	AAV19659
42	13	65.0	18	16	AAQ86659
43	13	65.0	18	19	AAV52545
44	13	65.0	18	19	AAV27719
45	13	65.0	18	19	AAV28181

ALIGNMENTS

RESULT 1	AAQ86649/c	AAQ86649 standard; DNA; 20 BP.
ID	AAQ86649	
XX	AAQ86649	
AC	AAQ86649	
DT	27-SEP-1995 (first entry)	
XX		
DE	Bcl-2 translation initiation site region.	
XX	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;	
KW	Lymphoma; programmed cell death; ss.	
KW		
OS	Synthetic.	
XX		
PN	W09508350-A.	
XX		
PD	30-MAR-1995.	
XX		
PF	20-SEP-1994; 94MO-US10725.	
XX		
PR	20-SEP-1993; 93US-0124256.	
XX		
PA	(REED/) REED J C.	
XX		
PI	Reed JC;	
XX		
DR	WPI; 1995-139394/18.	
XX		
PT	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment	
PT	of human solid tumours, esp. breast cancer	
XX		

Bcl-2 antisense ol
Bcl-2 translation
Human bcl-2 oligon
Human bcl-xl and b
Liposomal bcl-2 an
Human bcl genes an
Human bcl-2 antis
Antisense oligomer
Human bcl-2 antis
Human amino acid c
Human Bcl-2 mRNA t
Human Bcl-2 mRNA t
Human bcl-2 antis
Human bcl-2 PCR pr
PCR primer used to
PCR primer used to
PCR primer used to
Human Bcl-2 forwar
Human secreted pro
Capture oligonucle
Capture oligonucle
HCY primer used in
HCY primer used in
Human clone c92784
Human clone c92784
Human clone c92784
Human clone c92784
Human silent SNP c
Human silent SNP c
Human silent nonco
Immunostimulatory
Human bcl-2 antis
Bcl-2 antisense ol
Immunostimulatory
Antisense oligonuc

PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ8650-55) or the 5'-cap
CC region (AAQ8656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence
CC (AAQ86649) was used as a control.
XX
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 cagcgtgcgcacccctccc 20
20 CAGCGTGCGCCATCCTTCCC 1

RESULT 2
AAV19651
ID AAV19651 standard; DNA; 20 BP.
XX
AC AAV19651;
XX
XX 12-JUN-1998 (first entry)
DE Human bcl-2 antisense oligonucleotide 1.
XX
KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
XX cancer; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN US5734033-A.
XX
PD 31-MAR-1998.
XX
PF 24-MAR-1994; 94US-0288692.
XX
XX 21-FEB-1992; 92US-0840716.
PR 22-DEC-1988; 88US-0288692.
PR 24-MAR-1994; 94US-0217082.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
PA
XX
PI Reed J;
XX
PT WPI; 1998-229881/20.
XX
XX Antisense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
XX
XX
PS Claim 6; Columns 3-4; 21pp; English.
XX
XX This antisense oligonucleotide is complementary to the translation
XX initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
XX oligonucleotides are phosphorothioate derivatives and can straddle
XX strategic sites such as the translation initiation site, donor and
XX acceptor splicing sites, or sites for transportation or degradation.
XX Blocking translation at such strategic sites prevents the formation of
XX a functional bcl-2 gene product. These oligonucleotides may be used for
XX treating cancers associated with high levels of bcl-2 gene expression,
XX especially lymphomas and some leukaemias.
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 cagcgtgcgcacccctccc 20
20 CAGCGTGCGCCATCCTTCCC 1

RESULT 4
AAD15276
ID AAD15276 standard; DNA; 20 BP.
XX
AC AAD15276;
XX
XX 15-NOV-2001 (first entry)

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cagcgtgcgcacccctccc 20
1 cagcgtgcgcacccctccc 20
Db 1 cagcgtgcgcacccctccc 20
20 CAGCGTGCGCCATCCTTCCC 1

RESULT 3
AAV19657/C
ID AAV19657 standard; DNA; 20 BP.
XX
AC AAV19657;
XX
XX 12-JUN-1998 (first entry)
DE Human bcl-2 transcription initiation sense (TI-S) oligonucleotide.
XX
KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
XX cancer; ss.
XX
OS Synthetic.
XX Homo sapiens.
XX
PN US5734033-A.
XX
PD 31-MAR-1998.
XX
PF 24-MAR-1994; 94US-0288692.
XX
XX 21-FEB-1992; 92US-0840716.
PR 22-DEC-1988; 88US-0288692.
PR 24-MAR-1994; 94US-0217082.
XX
XX (TYPE-) UNIV PENNSYLVANIA.
PA
XX
PI Reed J;
XX
PT WPI; 1998-229881/20.
XX
XX Antisense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
XX for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
XX
XX
PS Disclosure; Column 19; 21pp; English.
XX
XX This oligonucleotide is used as a control in measuring DNA fragmentation
XX as an indicator of bcl-2 antisense oligonucleotide mediated programmed
XX cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
XX straddle strategic sites such as the translation initiation site, donor
XX and acceptor splicing sites, or sites for transportation or degradation.
XX Blocking translation at such strategic sites prevents the formation of a
XX functional bcl-2 gene product. These oligonucleotides may be used for
XX treating cancers associated with high levels of bcl-2 gene expression,
XX especially lymphomas and some leukaemias.
XX
SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 cagcgtgcgcacccctccc 20
20 CAGCGTGCGCCATCCTTCCC 1

RESULT 4
AAD15276
ID AAD15276 standard; DNA; 20 BP.
XX
AC AAD15276;
XX
XX 15-NOV-2001 (first entry)

XX DE Human Bcl-2 mRNA targeted liposomal antisense oligonucleotide #1.
XX KW Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; antisense;
XX KW chronic lymphocytic leukaemia; plasma cell dyscrasia; cancer; pancreas;
XX KW breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
XX KW testes; skin; head; kidney; colon; immune disorder; liposome; ss.
XX OS Homo sapiens.
XX PN WO200160998-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US40159.
XX PR 18-FEB-2000; 2000US-0506979.
XX PA (TEXA) UNIV TEXAS SYSTEM.
XX PI Taitl AM, Lopez-Berestein G, Gutierrez-Puente Y;
XX DR WPI; 2001-529911/58.
XX PT Compositions comprising short antisense oligonucleotides and a lipid
XX PT component, useful for treating Bcl-associated diseases, e.g. cancer -
XX PS Example 1; Page 31; 63pp; English.
XX CC The invention relates to a liposomal composition of antisense
XX CC oligonucleotides targeted to the translation initiation site of human
XX CC Bcl-2 mRNA. The invention also relates to a method useful for treating
XX CC Bcl-associated diseases like cancer such as follicular and nonfollicular
XX CC lymphomas, chronic lymphocytic leukaemia and plasma cell dyscrasias;
XX CC solid tumours like those associated with breast, prostate, liver,
XX CC pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
XX CC stomach, kidney and colon cancer; and immune disorders. The present DNA
XX CC sequence is liposomal antisense oligonucleotide targeted to the
XX CC translation initiation site of human Bcl-2 mRNA. This antisense
XX CC oligonucleotide which is preferably composed of a nuclease resistant
XX CC backbone is able to inhibit the production of Bcl-2 protein.
XX SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
Db 1 cagcgtgcgcacatcctccc 20

RESULT 5
AADI2300/C
ID AADI2300 standard; DNA; 20 BP.
XX AC AADI2300;
XX DT 06-NOV-2001 (first entry)
XX DE AM-TIS sulphate-oligonucleotide to detect binding of charged species.
XX KW AM-TIS sulphate-oligonucleotide; DNA transfection; fluorophore;
XX KW biomolecule; charged species; lipid vesicle; ss.
XX OS unidentified.
XX FH key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER

FT FT /note="Optionally labelled with FITC
FT FT (fluoresceinisochoyanate)"
FT FT modified_base 1..20
FT FT /*tag= b
FT FT /mod_base= OTHER
XX FT /note= "Sulphate-Oligodeoxynucleotide"
XX PN WO200159156-A2.
XX PD 16-AUG-2001.
XX PF 09-FEB-2001; 2001WO-IL00134.
XX PR 10-FEB-2000; 2000US-0181693.
XX PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX PI Barenholz Y, Hirsch-Jerner D, Cohen R, Dagan A, Gatt S;
XX DR WPI; 2001-497084/54.
XX CC Determining binding of compounds to a surface, particularly of DNA to
XX CC transfection vesicle, using lipid-coupled fluorophore as pH- or
XX CC potential-sensitive probe -
XX PS Example 4; Page 20; 39pp; English.
XX CC The invention relates to a method for determining the binding of a
XX CC species at a surface, where binding alters the local pH or the surface
XX CC potential, by stable incorporation of a probe at the surface. Probe
XX CC consists of a pH- or potential-sensitive fluorophore attached to either
XX CC a steroid or a lipid having at least two alkyl or alkenyl chains of at
XX CC least 14 carbons. A change in fluorescence from fluorophore when a
XX CC species binds to, or is released from, the surface is detected.
XX CC The method is used for determining the extent of binding of species,
XX CC particularly a biomolecule (nucleic acid or protein) to a surface or its
XX CC release from the surface. Particularly the surface is a lipid vesicle
XX CC being used for DNA transfection or a cell membrane. The method is also
XX CC useful for monitoring transfection of DNA to cells, in vivo or in vitro.
XX CC The method is used for detecting both specific and non-specific
XX CC interactions at the surface. The lipid/steroid component ensures stable
XX CC incorporation of the probe, thus stable and reproducible observation of
XX CC interactions. The present DNA sequence is an AM-TIS sulphate-
XX CC oligodeoxynucleotide which is used to detect the binding of charged
XX CC species.
XX SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
Db 20 CAGCCTGCGGCATCCTTCCC 1

RESULT 6
AADI2301
ID AADI2301 standard; DNA; 20 BP.
XX AC AADI2301;
XX DT 06-NOV-2001 (first entry)
XX DE Bcl2-TIAS sulphate-oligonucleotide to detect binding of charged species.
XX KW Bcl2-TIAS sulphate-oligonucleotide; DNA transfection; fluorophore;
XX KW biomolecule; charged species; lipid vesicle; ss.
XX OS unidentified.

```

FH Key Location/Qualifiers
FT modified_base 1
FT FT /*tag= a
FT FT /mod_base= OTHER
FT FT /note= "optionally labelled with FITC
FT FT (fluoresceinisochoyanate)"
FT modified_base 1..20
FT FT /*tag= b
FT FT /mod_base= OTHER
FT FT /note= "Sulphate-Oligodeoxynucleotide"
XX
XX WO200159156-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-1100134.
XX
XX 10-FEB-2000; 2000US-0181693.
XX
XX (YISS ) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX
XX Barenholz Y, Hirsch-Ierner D, Cohen R, Dagan A, Gatt S;
XX WPI; 2001-497084/54.
XX
XX Determining binding of compounds to a surface, particularly of DNA to
XX transfection vesicle, using lipid-coupled fluorophore as pH- or
XX potential-sensitive probe
XX
XX Example 4; Page 20; 39pp; English.
XX
XX The invention relates to a method for determining the binding of a
XX species at a surface, where binding alters the local pH or the surface
XX potential, by stable incorporation of a probe at the surface. Probe
XX consists of a pH- or potential-sensitive fluorophore attached to either
XX a steroid or a lipid having at least two alkyl or alkenyl chains of at
XX least 14 carbons. A change in fluorescence from fluorophore when a
XX species binds to, or is released from, the surface is detected.
XX The method is used for determining the extent of binding of species,
XX particularly a biomolecule (nucleic acid or protein) to a surface or its
XX release from the surface. Particularly the surface is a lipid vesicle
XX being used for DNA transfection or a cell membrane. The method is also
XX useful for monitoring transfection of DNA to cells, in vivo or in vitro.
XX The method is used for detecting both specific and non-specific
XX interactions at the surface. The lipid/steroid component ensures stable
XX incorporation of the probe, thus stable and reproducible observation of
XX interactions. The present DNA sequence is an Bcl2-YIAS sulphate-
XX Oligodeoxynucleotide which is used to detect the binding of charged
XX species.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other:
XX
XX
XX Query Match 100.0%; Score 20; DB 22; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.5;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 cagcgtgcgcacccctccc 20
XX 1 cagcgtgcgcacccctccc 20
XX
XX
XX RESULT 7
XX AAF77808
XX ID AAF77808 standard; DNA; 20 BP.
XX
XX AAF77808;
XX
XX 29-MAY-2001 (first entry)
XX
XX BCL-2 antisense oligodeoxynucleotide.
XX
XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
XX
```

```

XX
XX Unidentified.
XX
XX OS
XX WO200113914-A1.
XX
XX PD
XX 01-MAR-2001.
XX
XX 22-AUG-2000; 2000WO-US22957.
XX
XX 24-AUG-1999; 99US-0379718.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
XX Farrell NP;
XX
XX WPI; 2001-257588/26.
XX
XX Delivering antisense oligodeoxynucleotide to cells for treating
XX cancers, involves forming a complex comprising the oligodeoxynucleotide
XX and a polynuclear platinum compound, and providing the complex to the
XX cells
XX
XX Example 1; Page 27; 52pp; English.
XX
XX The present invention relates to a method for delivering an antisense
XX oligodeoxynucleotide to cells. The method comprises forming a complex
XX comprising the antisense oligonucleotide and a polynuclear platinum
XX compound, and providing the complex to the cells. The present sequence is
XX an antisense oligonucleotide for BCL-2, which may be used in the present
XX invention. BCL-2 is a suppressor of apoptosis and its expression in
XX cancer cells may contribute to the resistance of cancer cells to
XX apoptosis. The complex of the present invention is useful for treating
XX cancer and any other disease amenable to the treatment by antisense
XX oligonucleotides.
XX
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other:
XX
XX
XX Query Match 100.0%; Score 20; DB 22; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.5;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 cagcgtgcgcacccctccc 20
XX 1 cagcgtgcgcacccctccc 20
XX
XX
XX RESULT 8
XX AAF77809/C
XX ID AAF77809 standard; DNA; 20 BP.
XX
XX AAF77809;
XX
XX 29-MAY-2001 (first entry)
XX
XX Control sense oligodeoxynucleotide.
XX
XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
XX
XX Unidentified.
XX
XX WO200113914-A1.
XX
XX 01-MAR-2001.
XX
XX 22-AUG-2000; 2000WO-US22957.
XX
XX 24-AUG-1999; 99US-0379718.
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH.
XX
XX Farrell NP;
XX
```

DR WPI: 2001-257588/26.

xx Delivering antisense oligodeoxynucleotide to cells for treating

PT cancers, involves forming a complex comprising the oligodeoxynucleotide

PT and a polynuclear platinum compound, and providing the complex to the

PT cells

PS

PS Example 4; Page 28; 52pp; English.

XX

CC The present invention relates to a method for delivering an antisense

CC oligodeoxynucleotide to cells. The method comprises forming a complex

CC comprising the antisense oligonucleotide and a polynuclear platinum

CC compound, and providing the complex to the cells. The present sequence is

CC a control sense oligonucleotide which was used in an assay for BCL-2

CC antisense oligonucleotide activity (see AAF77808). BCL-2 is a suppressor

CC of apoptosis and its expression in cancer cells may contribute to the

CC resistance of cancer cells to apoptosis. The complex of the present

CC invention is useful for treating cancer and any other disease amenable to

CC the treatment by antisense oligonucleotides.

XX

SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 20; DB 22; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgctgcgcacatcctccc 20
|||||

DB 20 CAGCGTGCGCCATCCTCCC 1

RESULT 9

AAQ49816

ID AAQ49816 standard; DNA; 22 BP.

XX

AC AAQ49816;

XX

DT 03-MAY-1994 (first entry)

XX

DE BCL-2 antisense oligonucleotide.

XX

KM Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;

XX expression; myc; ss.

OS Synthetic.

XX

XX WO9320200-A.

PM

PD 14-OCT-1993.

XX

XX 02-APR-1993; 93WO-GB00686.

PF

XX 02-APR-1992; 92GB-0007275.

PR

XX 02-APR-1992; 92GB-0007276.

XX

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

XX

PI Evan GI;

XX

DR WPI: 1993-336908/42.

XX

XX Treating tumour cells by de-inhibiting Myc-induced apoptosis -

PT esp. by inhibiting expression of the BCL-2 oncogene e.g. with

PT antisense oligo:nucleotide(s), also increasing survival of

PT cultured cells by expressing BCL-2

XX

XX Disclosure; Page 58; 109pp; English.

XX

CC A DNA construct comprising the bcl-2 coding sequence under control

CC of elements allowing its expression is claimed. Myc-induced cell

CC death can be inhibited in cultured cells by expressing bcl-2.

CC Myc-induced cell death can be de-inhibited in tumour cells by admin.

```

CC of bcl-2 antisense oligonucleotides.
xx
SO Sequence 22 BP; 2 A; 12 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
   |||||
DB 3 cagcgtgcgcacatcctccc 22

RESULT 10
AAQ49817
ID AAQ49817 standard; RNA; 22 BP.
AC AAQ49817;
DT 03-MAY-1994 (first entry)
XX
DE Bcl-2 antisense oligonucleotide.
XX
KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW expression; myc; ss.
XX
OS Synthetic.
XX
PN W09320200-A.
XX
PD 14-OCT-1993.
XX
PF 02-APR-1993; 93WO-GB00686.
XX
PR 02-APR-1992; 92GB-0007275.
PR 02-APR-1992; 92GB-0007276.
XX
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
XX
PI
PI Evan GI;
XX
DR WPI; 1993-336908/42.
XX
PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing BCL-2
XX
PS Disclosure; Page 58; 109pp; English.
XX
CC A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC of bcl-2 antisense oligonucleotides.
XX
SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 U; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 22;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 16; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
   |||||
DB 3 cagcgtgcgcacacuuucc 22

RESULT 11
AAQ86644/c
ID AAQ86644 standard; DNA; 35 BP.
XX

```

AC AA086644;
XX
DE 27-SEP-1995 (first entry)
XX
DE Bcl-2 translation initiation region.
XX
KW Antisense oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
KW ss.
OS Synthetic.
XX
PN WO9508350-A.
XX
PD 30-MAR-1995.
XX
PF 20-SEP-1994; 94WO-US10725.
XX
PR 20-SEP-1993; 93US-0124256.
XX
PA (REED/) REED J C.
XX
PI Reed JC;
XX
DR WPI; 1995-139394/18.
XX
PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours; esp. breast cancer
XX
PS Disclosure; Page 13; 108pp; English.
XX
CC The antisense oligonucleotide TI-AS (AA086643) straddles the
CC translation-initiation site in the mRNA coding strand of the human
CC bcl-2 gene and is complementary to this region. It reduces the
CC expression of bcl-2 gene product thereby inducing programmed cell
CC death of certain cancer cells. The corresp. sense bcl-1 sequence
CC was synthesized for use as a control.
XX
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
DB 30 CAGCGTGCACATCCTTCCC 11

RESULT 12
AAV19652/C
ID AAV19652 standard; DNA; 35 BP.
XX
XX AAV19652;
XX
DE 12-JUN-1998 (first entry)
XX
DE Human bcl-2 oligonucleotide 1.
XX
KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukemia; human;
KW cancer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5734033-A.
XX
PD 31-MAR-1998.
XX
PF 24-MAR-1994; 94US-0288692.
XX
PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.
PR 24-MAR-1994; 94US-0217082.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Reed J;
XX
DR WPI; 1998-229881/20.
XX
PT Anti-sense oligo(nucleotide(s) complementary to BCL-2 mRNA - useful
PT for treating cancers, e.g. lymphoma(s) and some leukemia(s)
XX
XX Claim 1; Columns 3-4; 21pp; English.
XX
CC This is a human bcl-2 oligonucleotide based on which an antisense
CC oligonucleotide complementary to the translation initiation site of the
CC human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
CC straddle strategic sites such as the translation initiation site, donor
CC and acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukemias.
XX
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
DB 30 CAGCGTGCACATCCTTCCC 11

RESULT 13
AAC86407
ID AAC86407 standard; RNA; 20 BP.
XX
XX AAC86407;
XX
DE 28-FEB-2001 (first entry)
XX
DE Human bcl-XL and bcl-2 mRNA antisense control sequence C02.
XX
XX Human; bcl-XL; bcl-2; apoptosis; antisense; cancer; allergic disease;
XX restenosis; fibrosis; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO20006724-A2.
XX
PD 09-NOV-2000.
XX
PF 26-APR-2000; 2000WO-EP03708.
XX
PR 30-APR-1999; 99GB-0010119.
XX
PA (UYZU-) UNIV ZUERICH.
XX
PI Zangemeister-Wittke U, Luedke G, Huesken D;
XX
DR WPI; 2001-015981/02.
XX
XX Antisense oligonucleotide derivatives directed against human bcl-XL
XX mRNA and capable of modulating biosynthesis of human bcl-XL proteins,
XX useful in treatment and diagnosis of hyperproliferative diseases -
XX Example 2; Page 23; 38pp; English.
XX
CC The present invention provides antisense nucleotides which hybridise to
CC the human bcl-XL and bcl-2 mRNA sequences. The bcl-XL and bcl-2 proteins

CC are involved in apoptosis, and the antisense strands can be used to
 CC inhibit them and possibly lead to cell death. The nucleic acids of the
 CC invention can be used in the treatment of cancer, particularly
 CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
 CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
 CC types of allergic disease.

SO Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 95.0%; Score 19; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4.7;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcttc 19
 |||||
 Db 2 cagcgtgcgcacatcttc 20

RESULT 14

ID AAV11591 standard; DNA; 18 BP.

AC AAV11591;

DT 30-JUL-1998 (first entry)

DE Liposomal bcl-2 antisense polynucleotide.

KW Bcl-2; antisense; disease; treatment; cancer; follicular lymphoma;
 KW leukemia; plasma cell dyscrasia; breast; prostate; colon;
 KW autoimmune diseases; ss.

OS Synthetic.

OS Homo sapiens.

PN W09814172-A1.

PD 09-APR-1998.

PF 03-OCT-1997; 97WO-US18348.

PR 04-OCT-1996; 96US-0726211.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Lopez-Berestein G, McDonnell TJ, Tara AM, Tormo M;

DR WPI; 1998-239841/21.

PT Composition comprising oligo:nucleotide anti-sense to Bcl-2 gene -
 PT useful for, e.g. treatment of Bcl-2 related disease such as
 PT follicular lymphoma and auto-immune disease

PS Claim 4; Page 30; 69pp; English.

CC This sequence is a nuclease-resistant p-ethoxy antisense oligonucleotide
 CC which specifically binds to the translation initiation site of human
 CC bcl-2 mRNA. This oligonucleotide can be used in a method to treat Bcl-2
 CC related disease in humans and animals, e.g. cancer especially follicular
 CC lymphoma (FL), leukemia, plasma cell dyscrasia, cancer of breast,
 CC prostate and colon, or autoimmune diseases.

SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 90.0%; Score 18; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcttc 18
 |||||
 Db 1 cagcgtgcgcacatcttc 18

RESULT 15

ID AAC65064 standard; DNA; 21 BP.

AC AAC65064;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #8.

KW Antisense oligonucleotide; RNA molecule cleavage; immune activation;
 KW bcl; protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

PN W0200061810-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09293.

PR 08-APR-1999; 99US-0128377.

PA (OASI-) OASIS BIOSCIENCES INC.

PI Brown BD, Riley TA;

DR WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal
 PT bases, and modified backbone linkages is useful to target therapeutic
 PT genes, preferably anti-apoptosis or chemoresistance genes

PS Example 7; Fig 3; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides
 CC containing a number of degenerate bases and with a modified backbone
 CC which can be used to direct cleavage of target RNA molecules. The use of
 CC degenerate bases reduces the risk of immune activation following
 CC injection into animals, which causes deleterious side effects associated
 CC with many therapeutic antisense oligonucleotides. Sequences
 CC AAC65029-C65077 are antisense oligonucleotides and PCR primers used in
 CC assays to demonstrate the effects of the sequences of the invention.

SO Sequence 21 BP; 2 A; 9 C; 4 G; 4 T; 2 other;

Query Match 88.0%; Score 17.6; DB 21; Length 21;
 Best Local Similarity 89.5%; Pred. No. 22;
 Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcttc 19
 |||||
 Db 3 cagcgtgcgcacatcttc 21

Search completed: June 28, 2002, 22:40:01
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Mon Jul 1 08:40:43 2002

us-09-709-170a-1.szm75.rng

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 19:58:54 ; Search time 334.55 Seconds
(without alignments)
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Title: US-09-709-170A-1

Perfect score: 20

Sequence: 1 cagcgtgcgcacatccctccc 20

Scoring table: IDENTITY_NUC

Searched: Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2-6/ptodata/1/ina/6B.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	1 US-08-217-082A-1	Sequence 1, Appl
2	20	100.0	20	1 US-08-217-082A-7	Sequence 7, Appl
3	20	100.0	20	2 US-08-465-485A-1	Sequence 1, Appl
4	20	100.0	20	2 US-08-465-485A-7	Sequence 7, Appl
5	20	100.0	20	3 US-09-080-285-1	Sequence 1, Appl
6	20	100.0	20	3 US-09-080-285-7	Sequence 7, Appl
7	20	100.0	20	4 US-09-379-718-1	Sequence 1, Appl
8	20	100.0	20	4 US-09-379-718-2	Sequence 2, Appl
9	20	100.0	35	1 US-08-217-082A-2	Sequence 2, Appl
10	20	100.0	35	1 US-08-465-485A-2	Sequence 2, Appl
11	20	100.0	35	3 US-09-080-285-2	Sequence 2, Appl
12	17	85.0	17	1 US-08-217-082A-11	Sequence 11, Appl
13	16	80.0	17	1 US-08-217-082A-10	Sequence 10, Appl
14	15	75.0	17	1 US-08-217-082A-12	Sequence 12, Appl
15	13.6	68.0	27	1 US-08-410-804-13	Sequence 13, Appl
16	13.6	68.0	27	1 US-08-607-269-8	Sequence 8, Appl
17	13.6	68.0	27	1 US-08-259-514-13	Sequence 13, Appl
18	13.6	68.0	27	2 US-08-858-311-13	Sequence 13, Appl
19	13.6	68.0	27	2 US-08-858-311-13	Sequence 13, Appl
20	13.2	66.0	47	4 US-08-869-380-5	Sequence 5, Appl
21	13.2	66.0	47	4 US-08-869-380-7	Sequence 7, Appl
22	13.2	66.0	47	5 PCT-US95-13552-16	Sequence 16, Appl
23	13.2	66.0	47	5 PCT-US95-13552-18	Sequence 18, Appl
24	13.2	66.0	17	1 US-08-217-082A-9	Sequence 9, Appl
25	13	65.0	18	1 US-08-217-082A-17	Sequence 17, Appl
26	13	65.0	18	2 US-08-465-485A-17	Sequence 17, Appl
27	13	65.0	18	2 US-08-465-485A-24	Sequence 24, Appl

28	13	65.0	18	3 US-09-080-285-17	Sequence 17, Appl
29	13	65.0	18	3 US-09-080-285-24	Sequence 24, Appl
30	13	65.0	18	3 US-09-249-730-218	Sequence 218, Appl
31	13	65.0	18	3 US-09-118-220-1	Sequence 1, Appl
32	13	65.0	18	3 US-08-738-652-55	Sequence 55, Appl
33	13	65.0	18	4 US-09-030-701-27	Sequence 27, Appl
34	13	65.0	18	4 US-09-286-098-59	Sequence 59, Appl
35	13	65.0	18	4 US-09-286-098-104	Sequence 104, Appl
36	13	65.0	18	4 US-08-960-774-45	Sequence 45, Appl
37	13	65.0	18	4 US-09-078-954-14	Sequence 14, Appl
38	13	65.0	19	6 5276019-8	Patent No. 5276019
39	13	65.0	20	4 US-09-082-649B-60	Sequence 60, Appl
40	12.8	64.0	20	3 US-09-418-640-84	Sequence 84, Appl
41	12.6	63.0	32	4 US-09-272-496-5	Sequence 5, Appl
42	12.4	62.0	45	4 US-08-358-627F-1	Sequence 1, Appl
43	12.2	61.0	21	4 US-09-485-636-25	Sequence 25, Appl
44	12.2	61.0	30	5 PCT-US94-10257A-37	Sequence 37, Appl
45	12.2	61.0	33	3 US-08-816-346-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-08-217-082A-1

Sequence 1, Application US/08217082A

Patent No. 5734033

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 224 Airport Parkway

CITY: San Jose

STATE: California

COUNTRY: U.S.A.

ZIP: 95110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,082A

FILING DATE: 24-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ. ID NO. 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: Synthetic DNA

ANTI-SENSE: YES

US-08-217-082A-1

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 1 CAGCGTGCACCATCTTCCC 20

RESULT 2
US-08-217-082A-7/C
; Sequence 7, Application US/08217082A
; Patent No. 5734033

GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITTING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: Synthetic DNA
; ANTI-SENSE: NO

US-08-217-082A-7

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 20 CAGCGTGCACCATCTTCCC 1

RESULT 3
US-08-465-485A-1
; Sequence 1, Application US/08465485A

Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES

US-08-465-485A-1

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatcctccc 20
|||||
Db 1 CAGCGTGCACCATCTTCCC 20

RESULT 4
US-08-465-485A-7/C
; Sequence 7, Application US/08465485A
; Patent No. 5831066

GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-7

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 cagcgtgcgcacatcctccc 20
DB 20 CAGCGTGCACATCCTCC 1
RESULT 5
US-09-080-285-1
Sequence 1, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
DB 1 CAGCGTGCACATCCTCC 20

RESULT 6
US-09-080-285-7/c
Sequence 7, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-7

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
|||||
DB 20 CAGCGTGCACCATCCTCCC 1

RESULT 7
US-09-379-718-1
Sequence 1, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
TITLE OF INVENTION: Antisense Technology
FILE REFERENCE: Farrell/Kloster
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotides for gene therapy
US-09-379-718-1

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
|||||
DB 1 cagcgtgcgcacatcctccc 20

RESULT 8
US-09-379-718-2/c
Sequence 2, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
TITLE OF INVENTION: Antisense Technology
FILE REFERENCE: Farrell/Kloster
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: oligonucleotides for gene therapy
US-09-379-718-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cagcgtgcgcacatcctccc 20
|||||
DB 20 CAGCGTGCACCATCCTCCC 1

RESULT 9
US-08-217-082A-2/c
Sequence 2, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-2

Query Match 100.0%; Score 20; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacccctcc 20
Db 30 CAGCGTGCGCACCTCTCC 11

RESULT 10
US-08-465-485A-2/c

Sequence 2, Application US/08465485A

Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,485A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

US-08-465-485A-2

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 35;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacccctcc 20

Db 30 CAGCGTGCGCACCTCTCC 11

RESULT 11

US-09-080-285-2/c

Sequence 2, Application US/09080285

Patent No. 6040181

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

US-09-080-285-2

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 35;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacccctcc 20

Db 30 CAGCGTGCGCACCTCTCC 11

RESULT 12

US-08-217-082A-11

Sequence 11, Application US/08217082A

Patent No. 5734033

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 224 Airport Parkway

CITY: San Jose

STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-11

Query Match 85.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gcgtgcgcacatcttc 19
|||||
Db 1 GCGTGCACATCCTTC 17

RESULT 13
US-08-217-082A-10
Sequence 10, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLO, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-10

Query Match 80.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cagcgtgcgcacatct 16
|||||
Db 2 CAGCGTGCACATCCT 17

RESULT 14
US-08-217-082A-12
Sequence 12, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLO, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:

Search completed: June 28, 2002, 22:16:38
Job time: 8264 sec

SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-12

Query Match

Best Local Similarity 75.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 tgcgcacatcttccc 20
Db 1 TGCGCATCTTCCC 15

RESULT 15

US-08-410-804-13/C
Sequence 13, Application US/08410804
Patent No. 5632994
GENERAL INFORMATION:
APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410.804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-410-804-13

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 1; Length 27;
Matches 16; Conservative 80.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 cagcgtgcgcacatcttccc 20
Db 20 CAGCGTGC GCATGATTC 1

Mon Jul 1 08:40:44 2002

us-09-709-170a-1.szlm75.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:10:44 ; Search time 3762.88 seconds

(without alignments)
194.646 Million cell updates/sec

Title: US-09-709-170A-2

Perfect score: 35

Sequence: 1 ctttcctctgggaagatgctgcacacgtggaga 35

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_ov:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	35	100.0	35	6	AR052604
2	35	100.0	35	6	196083
3	22	62.9	22	6	A76123
4	22	62.9	22	6	A76124
5	20	57.1	20	6	AR052603
6	20	57.1	20	6	AR052609
7	20	57.1	20	6	AR176022
8	20	57.1	20	6	AR176023
9	20	57.1	20	6	AX045387
10	20	57.1	20	6	AX211669
11	20	57.1	20	6	AX211670
12	20	57.1	20	6	AX277461
13	20	57.1	20	6	196082
14	20	57.1	20	6	196088
15	19	54.3	19	6	AX083694
16	18	53.1	27	6	AR004426
17	18	53.1	27	6	143661
18	18	53.1	27	6	186720
19	18	52.6	60	6	AX113708
20	18	52.6	70	6	AX113709
21	18	51.4	18	6	AR052619
22	18	51.4	18	6	AR052624
23	18	51.4	18	6	AR116926
24	18	51.4	18	6	AR140496
25	18	51.4	18	6	AR146347
26	18	51.4	18	6	AR146392
27	18	51.4	18	6	AR154716
28	18	51.4	18	6	AR167448
29	18	51.4	18	6	AX015198
30	18	51.4	18	6	AX020948
31	18	51.4	18	6	AX020954
32	18	51.4	18	6	AX040169
33	18	51.4	18	6	AX040403
34	18	51.4	18	6	AX063576
35	18	51.4	18	6	AX081353
36	18	51.4	18	6	AX083693
37	18	51.4	18	6	AX088930
38	18	51.4	18	6	AX103809
39	18	51.4	18	6	AX103862
40	18	51.4	18	6	AX103863
41	18	51.4	18	6	AX103899
42	18	51.4	18	6	AX105211
43	18	51.4	18	6	AX135635
44	18	51.4	18	6	AX283183
45	18	51.4	18	6	AX283250

ALIGNMENTS

RESULT 1	AR052604	Sequence 2	from patent US 5831066.	DNA	linear	PAT 29-SRP-1999
LOCUS	AR052604	35 bp				
DEFINITION	Sequence 2					
ACCESSION	AR052604					
VERSION	AR052604.1	GI:5975968				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 35)					
AUTHORS	Reed, J.C.					
TITLE	Regulation of bcl-2 gene expression					
JOURNAL	Patent: US 5831066-A2 03-NOV-1998;					
FEATURES	Location/Qualifiers					
SOURCE	1..35					
BASE COUNT	6 a	8 c	13 g	8 t		
ORIGIN						

Query Match 100.0%; Score 35; DB 6; Length 35;
Best local Similarity 100.0%; Pred. No. 0.00024;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cttctcctggaagatgagcagctgga 35
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Db 1 CTTTCTCTGGAGAGATGGCGACCTGGAGA 35

RESULT 2
196083
LOCUS Sequence 2 from patent US 5734033. 35 bp DNA linear PAT 01-DEC-1998
DEFINITION
ACCESSION 196083
VERSION 196083.1 GI:3940553
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..35
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 100.0%; Score 35; DB 6; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cttctcctggaagatgagcagctgga 35
|||||
Db 1 CTTTCTCTGGAGAGATGGCGACCTGGAGA 35

RESULT 3
A76123/c
LOCUS Sequence 3 from Patent WO9320200. 22 bp DNA linear PAT 19-OCT-1999
DEFINITION
ACCESSION A76123
VERSION A76123.1 GI:6088259
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 3 14-OCT-1993;
FEATURES IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
source 1..22
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

Query Match 62.9%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 gggaagatgagcagctgga 32
|||||
Db 22 GGGAAGAGATGGCGACGCTGG 1

RESULT 4
A76124/c
LOCUS Sequence 4 from Patent WO9320200. 22 bp DNA linear PAT 19-OCT-1999
DEFINITION

ACCESSION A76124
VERSION A76124.1 GI:6088260
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 4 14-OCT-1993;
FEATURES IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
source 1..22
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

Query Match 62.9%; Score 22; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 gggaagatgagcagctgga 32
|||||
Db 22 GGGAAGAGATGGCGACGCTGG 1

RESULT 5
AR052603/c
LOCUS Sequence 1 from patent US 5831066. 20 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR052603
VERSION AR052603.1 GI:5975967
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 1 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 gggaagatgagcagctgga 30
|||||
Db 20 GGGAAGAGATGGCGACGCTG 1

RESULT 6
AR052609
LOCUS Sequence 7 from patent US 5831066. 20 bp DNA linear PAT 29-SEP-1999
DEFINITION
ACCESSION AR052609
VERSION AR052609.1 GI:5975973
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 7 03-NOV-1998;
FEATURES Location/Qualifiers

source 1. 20
/organism="unknown"
BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcctg 30
|||||
1 GGGAAGATGCGCAGCCTG 20

RESULT 7
LOCUS AR176022 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6310047.
ACCESSION AR176022
VERSION AR176022.1 GI:17917321
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 1 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcctg 30
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20 GGGAAGATGCGCAGCCTG 1

RESULT 8
LOCUS AR176023 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6310047.
ACCESSION AR176023
VERSION AR176023.1 GI:17917322
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 2 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcctg 30

|||||
Db 1 GGGAAGATGCGCAGCCTG 20

RESULT 9
LOCUS AX045387/c 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 7 from Patent WO0066724.
ACCESSION AX045387
VERSION AX045387.1 GI:11343871
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 20)
AUTHORS Zangemeister-Wilke,U., Luedke,G. and Huesken,D.
TITLE Oligonucleotide derivatives directed against human bcl-xl and human bcl-2 mrna
JOURNAL Patent: WO 0066724-A 7 09-NOV-2000;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Antisense"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 gggaagatgagcagcctg 31
|||||
20 GGGAAGATGCGCAGCCTG 1

RESULT 10
LOCUS AX211669 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 1 from Patent WO0159156.
ACCESSION AX211669
VERSION AX211669.1 GI:15523901
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatl,S.
TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 1 16-AUG-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note=""

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcctg 30
|||||
1 GGGAAGATGCGCAGCCTG 20

RESULT 11
AX211670/c
LOCUS AX211670 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 2 from Patent WO0159156.
ACCESSION AX211670
VERSION AX211670.1 GI:15523902
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
synthetic construct.
artificial sequence.
1 (bases 1 to 20)
Barenholz, Y., Hirsch-Ierner, D., Cohen, R., Dagan, A. and Galt, S.
Detection of binding of charged species using ph- or
potential-sensitive probes
Patent: WO 0159156-A 2 16-AUG-2001;
Yissum Research Development Co., the Hebrew University of Jerusalem
(IL)
FEATURES
SOURCE
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note=""
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGAAGATGGCGACGCTG 1

RESULT 12
AX277461/c
LOCUS AX277461 20 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 1 from Patent WO0160998.
ACCESSION AX277461
VERSION AX277461.1 GI:16548979
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
synthetic construct.
artificial sequence.
1 (sites)
Tari, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
Small oligonucleotides with anti-tumor activity
Patent: WO 0160998-A 1 23-AUG-2001;
Board of Regents, The University of Texas System (US)
FEATURES
SOURCE
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic primer"
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGAAGATGGCGACGCTG 1

RESULT 13
196082/c
LOCUS 196082 20 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 1 from patent US 5734033.
ACCESSION 196082

VERSION 196082.1 GI:3940552
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 20)
Reed, J.
Antisense oligonucleotides inhibiting human bcl-2 gene expression
Patent: US 5734033-A 1 31-MAR-1998;
Location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGAAGATGGCGACGCTG 1

RESULT 14
196088
LOCUS 196088 20 bp DNA linear PAT 01-DEC-1998
DEFINITION Sequence 7 from patent US 5734033.
ACCESSION 196088
VERSION 196088.1 GI:3940558
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
Unknown.
Unclassified.
1 (bases 1 to 20)
Reed, J.
Antisense oligonucleotides inhibiting human bcl-2 gene expression
Patent: US 5734033-A 7 31-MAR-1998;
Location/Qualifiers
1..20
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BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 57.1%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 11 gggaagatggcgacgctg 30
|||||
Db 1 GGAAGATGGCGACGCTG 20

RESULT 15
AX083694/c
LOCUS AX083694 19 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 8 from Patent WO0110468.
ACCESSION AX083694
VERSION AX083694.1 GI:13185422
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
synthetic construct.
artificial sequence.
1 (bases 1 to 19)
Papisov, M.I.
Drug-carrier complexes and methods of use thereof
Patent: WO 0110468-A 8 15-FEB-2001;
THE GENERAL HOSPITAL CORPORATION (US)
Location/Qualifiers
1..19
/organism="synthetic construct"
FEATURES
SOURCE

/db_xref="taxon:32630"
 /note="Synthetic Oligonucleotide-c indicates an RNA base"
 BASE COUNT 2 a 9 c 4 g 4 t
 ORIGIN

Query Match 54.3%; Score 19; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 gatggcgacgcgtggaga 35
 ||||||||||||||||
 Db 19 GATGGCGCACGCTGGGAGA 1

Search completed: June 28, 2002, 22:10:45
 Job time: 8336 sec

	RESULT
XX	1
XX	AAQ86644
XX	AAQ86644 standard; DNA; 35 BP.
XX	AAQ86644;
XX	27-SEP-1995 (first entry)
XX	Bcl-2 translation initiation region.
XX	Anticod oligomer: antisense oligonucleotide; bcl-2; cancer; therapy
XX	leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
XX	ss.
XX	Synthetic.
XX	OS
XX	WO9508350-A.
XX	PN
XX	30-MAR-1995.
XX	PD
XX	20-SEP-1994; 94WO-US10725.
XX	PF
XX	20-SEP-1993; 93US-0124256.
XX	PR
XX	(REED/) REED J C.
XX	PA
XX	Reed JC;
XX	PI
XX	DR
XX	WPI; 1995-139394/18.
XX	PT
XX	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
XX	of human solid tumours, esp. breast cancer

XX Disclosure; Page 13; 108pp; English.
PS
XX
CC The antisense oligonucleotide T1-AS (AAQ86643) straddles the
CC translation-initiation site in the mRNA coding strand of the human
CC bcl-2 gene and is complementary to this region. It reduces the
CC expression of bcl-2 gene product thereby inducing programmed cell
CC death of certain cancer cells. The corresp. sense bcl-1 sequence
CC was synthesized for use as a control.
XX
SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match 100.0%; Score 35; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cttctctcgggaagatgagcagcctgggaga 35
1 cttctctcgggaagatgagcagcctgggaga 35
Db

RESULT 2

AAV19652
ID AAV19652 standard; DNA: 35 BP.

AC AAV19652;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 1.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

OS Homo sapiens.

PN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Claim 1: Columns 3-4; 21pp; English.
XX
XX This is a human bcl-2 oligonucleotide based on which an antisense
CC oligonucleotide complementary to the translation initiation site of the
CC human bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides
CC straddle strategic sites such as the translation initiation site, donor
CC and acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.

SQ Sequence 35 BP; 6 A; 8 C; 13 G; 8 T; 0 other;

Query Match

100.0%; Score 35; DB 19; Length 35;

Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cttctctcgggaagatgagcagcctgggaga 35
1 cttctctcgggaagatgagcagcctgggaga 35
Db

RESULT 3

AAQ49816/C
ID AAQ49816 standard; DNA: 22 BP.

AC AAQ49816;

DT 03-MAY-1994 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;

KW expression; myc; ss.

OS Synthetic.

PN W03320200-A.

PD 14-OCT-1993.

PF 02-APR-1993; 93WO-GB00686.

PR 02-APR-1992; 92GB-0007275.

PR 02-APR-1992; 92GB-0007276.

PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.

PI Evan GT;

DR WPI; 1993-336908/42.

PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT esp. by inhibiting expression of the bcl-2 oncogene e.g. with
PT antisense oligo:nucleotide(s), also increasing survival of
PT cultured cells by expressing BCL-2

PS Disclosure; Page 58; 109pp; English.

XX
XX A DNA construct comprising the bcl-2 coding sequence under control
CC of elements allowing its expression is claimed. Myc-induced cell
CC death can be inhibited in cultured cells by expressing bcl-2.
CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC of bcl-2 antisense oligonucleotides.

SQ Sequence 22 BP; 2 A; 12 C; 4 G; 4 T; 0 other;

Query Match 62.9%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 gggaagatgagcagcctggg 32
22 GGGAAGATGAGCAGCCTGGG 1
Db

RESULT 4

AAQ49817/C
ID AAQ49817 standard; RNA: 22 BP.

AC AAQ49817;

DT 03-MAY-1994 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
 KM expression; myc; ss.
 XX Synthetic.
 OS
 PN W09320200-A.
 XX
 PD 14-OCT-1993.
 XX
 PF 02-APR-1993; 93WO-GB00686.
 XX
 PR 02-APR-1992; 92GB-0007275.
 PR 02-APR-1992; 92GB-0007276.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PI Evan GI;
 XX
 DR WPI; 1993-336908/42.
 XX
 PT Treating tumour cells by de-inhibiting Myc-induced apoptosis -
 PT esp. by inhibiting expression of the Bcl-2 oncogene e.g. with
 PT antisense oligo:nucleotide(s), also increasing survival of
 PT cultured cells by expressing Bcl-2
 XX
 PS Disclosure: Page 58; 109pp; English.
 XX
 CC A DNA construct comprising the bcl-2 coding sequence under control
 CC of elements allowing its expression is claimed. Myc-induced cell
 CC death can be inhibited in cultured cells by expressing bcl-2.
 CC Myc-induced cell death can be de-inhibited in tumour cells by admin.
 CC of bcl-2 antisense oligonucleotides.
 CC
 XX Sequence 22 BP; 2 A; 12 C; 4 G; 4 U; 0 other;
 SQ
 Query Match 62.9%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 gggaagatgagcagcagctgg 32
 22 GCGAAGATGCGCGCCGCTGGG 1
 Db
 RESULT 5
 AA086649
 ID AA086649 standard; DNA; 20 BP.
 XX
 AC AA086649;
 XX
 DT 27-SEP-1995 (first entry)
 DE Bcl-2 translation initiation site region.
 XX
 KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 KW lymphoma; programmed cell death; ss.
 XX
 OS Synthetic.
 XX
 PN W09508350-A.
 XX
 PD 30-MAR-1995.
 XX
 PF 20-SEP-1994; 94WO-US10725.
 XX
 PR 20-SEP-1993; 93US-0124256.
 XX
 PA (REED/) REED J C.
 XX
 PI Reed JC;
 XX
 DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Example 12; Page 33; 108pp; English.
 XX
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS1846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA086650-55) or the 5'-cap
 CC region (AA086656-58) of human bcl-2 pre-mRNAs. A bcl-2 sense sequence
 CC (AA086649) was used as a control.
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;
 Query Match 57.1%; Score 20; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 gggaagatgagcagcagctg 30
 1 gggaagatgagcagcagctg 20
 Db
 RESULT 6
 AA19651/C
 ID AA19651 standard; DNA; 20 BP.
 XX
 AC AA19651;
 XX
 DT 12-JUN-1998 (first entry)
 DE Human bcl-2 antisense oligonucleotide 1.
 XX
 KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;
 KW cancer; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5734033-A.
 XX
 PD 31-MAR-1998.
 XX
 PF 24-MAR-1994; 94US-0288692.
 XX
 PR 21-FEB-1992; 92US-0840716.
 PR 22-DEC-1988; 88US-0288692.
 PR 24-MAR-1994; 94US-0217082.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Reed J;
 XX
 DR WPI; 1998-229881/20.
 XX
 KW Antisense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 KW for treating cancers, e.g. lymphoma(s) and some leukaemia(s)
 XX
 OS Claim 6; Columns 3-4; 21pp; English.
 XX
 CC This antisense oligonucleotide is complementary to the translation
 CC initiation site of the human bcl-2 mRNA. The Bcl-2 antisense
 CC oligonucleotides are phosphorothioate derivatives and can straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of
 CC a functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 XX
 SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match
Best Local Similarity 57.1%; Score 20; DB 19; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ggaagagatgagcagcagctg 30
DB 20 GGGAGAGATGCGCAGCCTG 1

RESULT 7

AAV19657
AAV19657 standard; DNA; 20 BP.

AC AAV19657;

DE 12-JUN-1998 (first entry)

DE Human bcl-2 transcription initiation sense (T1-S) oligonucleotide.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukemia; human;

OS Synthetic.

OS Homo sapiens.

FN US5734033-A.

PD 31-MAR-1998.

PF 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
for treating cancers, e.g. lymphoma(s) and some leukemia(s)

PS Disclosure; Column 19; 21pp; English.

XX This oligonucleotide is used as a control in measuring DNA fragmentation
as an indicator of bcl-2 antisense oligonucleotide mediated programmed
cell death in human lymphoma cells. Bcl-2 antisense oligonucleotides
straddle strategic sites such as the translation initiation site, donor
and acceptor splicing sites, or sites for transportation or degradation.
Blocking translation at such strategic sites prevents the formation of a
functional bcl-2 gene product. These oligonucleotides may be used for
treating cancers associated with high levels of bcl-2 gene expression,
especially lymphomas and some leukemias.

XX Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match
Best Local Similarity 57.1%; Score 20; DB 19; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ggaagagatgagcagcagctg 30
DB 1 ggaagagatgagcagcagctg 20

RESULT 8

AAV15276/c
AAV15276 standard; DNA; 20 BP.

XX AAV15276;

DE 15-NOV-2001 (first entry)

DE Human Bcl-2 mRNA targeted liposomal antisense oligonucleotide #1.

KW Human; Bcl-2 protein; cytostatic; lymphoma; cancer therapy; antisense;
chronic lymphocytic leukemia; plasma cell dyscrasia; cancer; pancreas;
breast; liver; lung; brain; ovary; stomach; prostate; neck; oesophagus;
testes; skin; head; kidney; colon; immune disorder; liposome; ss.

OS Homo sapiens.

FN WO200160998-A2.

PD 23-AUG-2001.

PF 20-FEB-2001; 2001WO-0540159.

PR 18-FEB-2000; 2000US-0506979.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Tari AM, Lopez-Berestein G, Gutierrez-Puente Y;

DR WPI; 2001-529911/58.

PT Compositions comprising short antisense oligonucleotides and a lipid
component, useful for treating Bcl-associated diseases, e.g. cancer -

PS Example 1; Page 31; 63pp; English.

XX The invention relates to a liposomal composition of antisense
oligonucleotides targeted to the translation initiation site of human
Bcl-2 mRNA. The invention also relates to a method useful for treating
Bcl-associated diseases like cancer such as follicular and nonfollicular
lymphomas, chronic lymphocytic leukemia and plasma cell dyscrasias;
solid tumours like those associated with breast, prostate, liver,
pancreas, lung, brain, ovary, testes, skin, head, neck, oesophagus,
stomach, kidney and colon cancer; and immune disorders. The present DNA
sequence is liposomal antisense oligonucleotide targeted to the
translation initiation site of human Bcl-2 mRNA. This antisense
oligonucleotide which is preferably composed of a nuclease resistant
backbone is able to inhibit the production of Bcl-2 protein.

XX Sequence 20 BP; 2 A; 10 G; 4 C; 4 T; 0 other;

Query Match
Best Local Similarity 57.1%; Score 20; DB 22; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 ggaagagatgagcagcagctg 30
DB 20 GGGAGAGATGCGCAGCCTG 1

RESULT 9

AAV12300
AAV12300 standard; DNA; 20 BP.

AC AAV12300;

DE 06-NOV-2001 (first entry)

DE AM-TIS sulphate-oligonucleotide to detect binding of charged species.

KW AM-TIS sulphate-oligonucleotide; DNA transfection; fluorophore;
biomolecule; charged species; lipid vesicle; ss.

OS Unidentified.

XX

XX BCL-2 antisense oligodeoxynucleotide.
 DE BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
 XX
 XX Unidentified.
 OS
 XX WO200113914-A1.
 PN
 XX
 XX 01-MAR-2001.
 PD
 XX
 XX 22-AUG-2000; 2000WO-US22957.
 PF
 XX
 XX 24-AUG-1999; 99US-0379718.
 PR
 XX
 XX (UYVI-) UNIV VIRGINIA COMMONWEALTH.
 PA
 XX
 XX Farrell NP;
 PI
 XX WPI; 2001-257588/26.
 DR
 XX
 XX Delivering antisense oligodeoxynucleotide to cells for treating
 PT cancers, involves forming a complex comprising the oligodeoxynucleotide
 PT and a polynuclear platinum compound, and providing the complex to the
 PT cells
 CC
 XX
 PS Example 1; Page 27; 52pp; English.

XX The present invention relates to a method for delivering an antisense
 CC oligodeoxynucleotide to cells. The method comprises forming a complex
 CC comprising the antisense oligonucleotide and a polynuclear platinum
 CC compound, and providing the complex to the cells. The present sequence is
 CC an antisense oligonucleotide for BCL-2, which may be used in the present
 CC invention. BCL-2 is a suppressor of apoptosis and its expression in
 CC cancer cells may contribute to the resistance of cancer cells to
 CC apoptosis. The complex of the present invention is useful for treating
 CC cancer and any other disease amenable to the treatment by antisense
 CC oligonucleotides.
 CC
 XX
 SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 57.1%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 44;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaagatgagcgacgctg 30
 |||||
 Db 20 GGGAAGATGGCGACGCTG 1

RESULT 12
 AAF77809
 ID AAF77809 standard; DNA; 20 BP.
 XX
 XX AAF77809;
 AC
 XX
 XX 29-MAY-2001 (first entry)
 DT
 XX
 XX Control sense oligodeoxynucleotide.
 DE
 XX BCL-2; apoptosis; cancer; cytostatic; antisense gene therapy; ss.
 KM
 XX Unidentified.
 OS
 XX WO200113914-A1.
 PN
 XX
 XX 01-MAR-2001.
 PD
 XX
 XX 22-AUG-2000; 2000WO-US22957.
 PF
 XX
 XX 24-AUG-1999; 99US-0379718.
 PR
 XX
 XX

PA (UYVI-) UNIV VIRGINIA COMMONWEALTH.
 XX
 XX Farrell NP;
 PI
 XX
 XX WPI; 2001-257588/26.
 DR
 XX
 XX Delivering antisense oligodeoxynucleotide to cells for treating
 PT cancers, involves forming a complex comprising the oligodeoxynucleotide
 PT and a polynuclear platinum compound, and providing the complex to the
 PT cells
 CC
 XX
 PS Example 4; Page 28; 52pp; English.

XX The present invention relates to a method for delivering an antisense
 CC oligodeoxynucleotide to cells. The method comprises forming a complex
 CC comprising the antisense oligonucleotide and a polynuclear platinum
 CC compound, and providing the complex to the cells. The present sequence is
 CC a control sense oligonucleotide which was used in an assay for BCL-2
 CC antisense oligonucleotide activity (see AAF77808). BCL-2 is a suppressor
 CC of apoptosis and its expression in cancer cells may contribute to the
 CC resistance of cancer cells to apoptosis. The complex of the present
 CC invention is useful for treating cancer and any other disease amenable to
 CC the treatment by antisense oligonucleotides.
 CC
 XX
 SQ Sequence 20 BP; 4 A; 4 C; 10 G; 2 T; 0 other;

Query Match 57.1%; Score 20; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. NO. 44;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaagatgagcgacgctg 30
 |||||
 Db 1 ggaagatgagcgacgctg 20

RESULT 13
 AAC86407/C
 ID AAC86407 standard; RNA; 20 BP.
 XX
 XX AAC86407;
 AC
 XX
 XX 28-FEB-2001 (first entry)
 DT
 XX
 XX Human bcl-xl and bcl-2 mRNA antisense control sequence CO2.
 DE
 XX
 XX Human: bcl-xl; bcl-2; apoptosis; antisense; cancer; allergic disease;
 KM restenosis; fibrosis; psoriasis; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200066724-A2.
 PN
 XX
 XX 09-NOV-2000.
 PD
 XX
 XX 26-APR-2000; 2000WO-EP03708.
 PF
 XX
 XX 30-APR-1999; 99GB-0010119.
 PR
 XX
 XX (UYZU-) UNIV ZUERICH.
 PA
 XX Zangemeister-Wittke U, Luedke G, Huesken D;
 PI
 XX
 XX WPI; 2001-015981/02.
 DR
 XX
 XX Antisense oligonucleotide derivatives directed against human bcl-xl
 PT mRNA and capable of modulating biosynthesis of human bcl-xl proteins,
 PT useful in treatment and diagnosis of hyperproliferative diseases -
 PT
 XX
 XX Example 2; Page 23; 38pp; English.
 PS
 XX
 XX The present invention provides antisense nucleotides which hybridise to
 CC the human bcl-xl and bcl-2 mRNA sequences. The bcl-xl and bcl-2 proteins

CC are involved in apoptosis, and the antisense strands can be used to
CC inhibit them and possibly lead to cell death. The nucleic acids of the
CC invention can be used in the treatment of cancer, particularly
CC colorectal, gastric, prostate, thyroid, renal, breast and lung cancers,
CC neuroblastoma and melanoma, restenosis, fibrosis, psoriasis and certain
CC types of allergic disease.
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 57.1%; Score 20; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 ggaagatgagcgcagctgg 31
|||||
DB 20 GGAGGATGGCGCAGCTGG 1

RESULT 14

AAC65064/C
ID AAC65064 standard; DNA; 21 BP.

AC AAC65064;

DT 12-FEB-2001 (first entry)

DE Human bcl genes antisense sequence #8.

KM Antisense oligonucleotide; RNA molecule cleavage; immune activation;
KW bcl; protein kinase C; PKC; PCR primer; ss.

OS Homo sapiens.

PN WO200061810-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09293.

PR 08-APR-1999; 99US-0128377.

PA (OASIS) OASIS BIOSCIENCES INC.

PI Brown BD, Riley TA;

DR WPI; 2000-679502/66.

PT Antisense oligonucleotides containing degenerate and/or universal
PT bases, and modified backbone linkages is useful to target therapeutic
PT genes, preferably anti-apoptosis or chemoresistance genes

PS Example 7; Fig 3; 32pp; English.

CC The present invention is concerned with antisense oligonucleotides
CC containing a number of degenerate bases and with a modified backbone
CC which can be used to direct cleavage of target RNA molecules. The use of
CC degenerate bases reduces the risk of immune activation following
CC injection into animals, which causes deleterious side effects associated
CC with many therapeutic antisense oligonucleotides. Sequences
CC AAC65029-C65077 are antisense oligonucleotides and PCR primers used in
CC assays to demonstrate the effects of the sequences of the invention.
XX

SQ Sequence 21 BP; 2 A; 9 C; 4 G; 4 T; 2 other;

Query Match 56.0%; Score 19; DB 21; Length 21;
Best Local Similarity 90.5%; Pred. No. 64;
Matches 19; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 ggaagatgagcgcagctgg 32
|||||
DB 21 GGAARNATGGCGCAGCTGG 1

RESULT 15

AAZ06730/C
ID AAZ06730 standard; DNA; 19 BP.

AC AAZ06730;

DT 23-NOV-1999 (first entry)

DE Antisense oligomer used to determine role of Bcl-2.

KM p75NTR; p75 neurotrophin receptor; nerve growth factor;

KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;

KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;

KW skin colour; alopecia areata; male pattern baldness; ss.

OS Synthetic.

PN Homo sapiens.

PD WO9939728-A2.

PF 12-AUG-1999.

PR 03-FEB-1999; 99WO-US02362.

PR 04-FEB-1998; 98US-0018194.

PA (UYBO-) UNIV BOSTON.

PI Eller M, Gilchrist BA, Yaar M;

DR WPI; 1999-539950/45.

PT Controlling or manipulating melanocyte and keratinocyte cell death,
PT useful for treating, e.g. alopecia areata

PS Example 8; Page 32; 67pp; English.

CC Sequences AAZ06728-706729 are used to determine the role of the p75
CC nerve growth factor receptor (p75-NGFR/p75NTR) in mediating nerve growth
CC factor survival effect in melanocytic cells. p75NTR is a low affinity
CC nerve growth factor (NGF) receptor which is expressed by melanocytes and
CC keratinocytes of the basal epidermis. Apoptosis can be inhibited by
CC p75NTR via the upregulation of the Bcl-2 protein. These oligomer
CC sequences were used to determine that if p75NTR is occupied by
CC appropriate ligands e.g. neurotrophins, apoptosis is inhibited via
CC Bcl-2. Other examples of appropriate ligands include the cyclic peptides
CC AAY39233-Y39235, which are based on the beta-amyloid sequence, which
CC binds to p75NTR in Alzheimer's disease. The cyclic peptides can be used
CC in methods to control or manipulate keratinocyte or melanocyte cell
CC death. The methods involve using the peptides to bind as a pseudo-ligand
CC to the p75 neurotrophin receptor, inhibiting apoptosis. The new method
CC can induce or maintain hair growth, hair colour or skin colour. Inducing
CC or maintaining hair growth is useful for treating alopecia areata or
CC male pattern baldness in vertebrates.
XX

SQ Sequence 19 BP; 2 A; 9 C; 4 G; 4 T; 0 other;

Query Match 54.3%; Score 19; DB 20; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 aagatgagcgcagctgg 32
|||||
DB 19 AAGGATGGCGCAGCTGG 1

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Mon Jul 1 08:40:53 2002

us-09-709-170a-2.szlm75.rng

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:38 ; Search time 334.55 seconds
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Title: US-09-709-170A-2

Perfect score: 35
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	35	100.0	35 1	US-08-217-082A-2
2	35	100.0	35 2	US-08-465-485A-2
3	35	100.0	35 3	US-09-080-285-2
4	20	57.1	20 1	US-08-217-082A-1
5	20	57.1	20 2	US-08-217-082A-7
6	20	57.1	20 2	US-08-465-485A-1
7	20	57.1	20 2	US-08-465-485A-7
8	20	57.1	20 3	US-09-080-285-1
9	20	57.1	20 3	US-09-080-285-7
10	20	57.1	20 4	US-09-379-718-1
11	20	57.1	20 4	US-09-379-718-2
12	18.6	53.1	27 1	US-08-410-804-13
13	18.6	53.1	27 1	US-08-607-269-8
14	18.6	53.1	27 1	US-08-559-514-13
15	18.6	53.1	27 2	US-08-858-311-13
16	18.6	53.1	27 5	PCT-US95-04600-8
17	18.6	53.1	18 1	US-08-217-082A-17
18	18.6	53.1	18 2	US-08-465-485A-17
19	18.6	53.1	18 3	US-08-465-485A-24
20	18.6	53.1	18 3	US-09-080-285-17
21	18.6	53.1	18 3	US-09-080-285-24
22	18.6	53.1	18 3	US-09-249-730-218
23	18.6	53.1	18 3	US-09-118-220-1
24	18.6	53.1	18 4	US-08-738-652-55
25	18.6	53.1	18 4	US-09-030-701-27
26	18.6	53.1	18 4	US-09-286-098-59
27	18.6	53.1	18 4	US-09-286-098-104

C 28	18	51.4	18 4	US-08-960-774-45	Sequence 45, Appl
C 29	18	51.4	18 4	US-09-078-954-14	Sequence 14, Appl
C 30	18	51.4	20 4	US-09-082-649B-60	Sequence 60, Appl
C 31	17	48.6	17 1	US-08-217-082A-9	Sequence 9, Appl
C 32	17	48.6	17 1	US-08-217-082A-10	Sequence 10, Appl
C 33	17	48.6	17 1	US-08-217-082A-11	Sequence 11, Appl
C 34	17	48.6	17 1	US-08-217-082A-12	Sequence 12, Appl
C 35	17	48.6	17 1	US-08-217-082A-13	Sequence 13, Appl
C 36	16.4	46.9	18 4	US-09-030-701-41	Sequence 41, Appl
C 37	16.4	46.9	18 4	US-09-030-701-60	Sequence 60, Appl
C 38	16.4	46.9	18 4	US-09-286-098-72	Sequence 72, Appl
C 39	16.4	46.9	18 4	US-08-960-774-72	Sequence 72, Appl
C 40	16.4	46.9	20 4	US-09-109-663-72	Sequence 72, Appl
C 41	15.8	45.1	40 1	US-08-231-342-12	Sequence 12, Appl
C 42	15.4	44.0	33 3	US-08-650-726-1	Sequence 1, Appl
C 43	15.4	44.0	70 1	US-08-434-001-109	Sequence 109, App
C 44	15.4	44.0	70 1	US-08-433-585-109	Sequence 109, App
C 45	15.4	44.0	70 1	US-08-434-425-109	Sequence 109, App

ALIGNMENTS

RESULT 1
US-08-217-082A-2
Sequence 2, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-2

Query Match 100.0%; Score 35; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cttctcctgtggaagatgagcagctgtggaga 35
|||||
Db 1 ctttctcctgtggaagatgagcagctgtggaga 35

RESULT 2

US-08-465-485A-2
; Sequence 2, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-465-485A-2

Query Match 100.0%; Score 35; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cttctcctgtggaagatgagcagctgtggaga 35
|||||
Db 1 ctttctcctgtggaagatgagcagctgtggaga 35

RESULT 3
US-09-080-285-2
; Sequence 2, Application US/09080285

; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-2

Query Match 100.0%; Score 35; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cttctcctgtggaagatgagcagctgtggaga 35
|||||
Db 1 ctttctcctgtggaagatgagcagctgtggaga 35

RESULT 4
US-08-217-082A-1/c
; Sequence 1, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.

STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-1

Query Match 57.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaagagatggcgacgctg 30
|||||
DB 20 GGAAGAGATGGCGACGCTG 1

RESULT 5
US-08-217-082A-7
Sequence 7, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994

CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: NO
US-08-217-082A-7

Query Match 57.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 ggaagagatggcgacgctg 30
|||||
DB 1 GGAAGAGATGGCGACGCTG 20

RESULT 6
US-08-465-485A-1/c
Sequence 1, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-1

Query Match 57.1%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 gggaagatgagcgacgctg 30
|||||
Db 20 GGAAGATGCGCACGCTG 1

RESULT 7
US-08-465-485A-7
Sequence 7, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-7

Query Match 57.1%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 gggaagatgagcgacgctg 30
|||||
Db 1 GGAAGATGCGCACGCTG 20

RESULT 8
US-09-080-285-1/c
Sequence 1, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-1

Query Match 57.1%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 gggaagatgagcgacgctg 30
|||||
Db 20 GGAAGATGCGCACGCTG 1

RESULT 9
US-09-080-285-7
; Sequence 7, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-7

Query Match 57.1%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatggcgacgctg 30
|||||
Db 1 GGAAGATGGCGACGCTG 20

RESULT 10
US-09-379-718-1/C
; Sequence 1, Application US/09379718
; Patent No. 6310047
; GENERAL INFORMATION:
; APPLICANT: Farrell, Nicholas
; APPLICANT: Kloster, Miriam

; TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
; FILE OF INVENTION: Antisense Technology
; FILE REFERENCE: farrell/kloster
; CURRENT APPLICATION NUMBER: US/09/379,718
; CURRENT FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-379-718-1

Query Match 57.1%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatggcgacgctg 30
|||||
Db 20 GGAAGATGGCGACGCTG 1

RESULT 11
US-09-379-718-2
; Sequence 2, Application US/09379718
; Patent No. 6310047
; GENERAL INFORMATION:
; APPLICANT: Farrell, Nicholas
; APPLICANT: Kloster, Miriam
; TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
; FILE OF INVENTION: Antisense Technology
; FILE REFERENCE: farrell/kloster
; CURRENT APPLICATION NUMBER: US/09/379,718
; CURRENT FILING DATE: 1999-08-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Oligonucleotides for gene therapy
; US-09-379-718-2

Query Match 57.1%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 gggaagatggcgacgctg 30
|||||
Db 1 gggaagatggcgacgctg 20

RESULT 12
US-08-410-804-13
; Sequence 13, Application US/08410804
; Patent No. 5632894
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cathryn Campbell
; STREET: 4370 La Jolla Village Drive, Ste 700
; CITY: San Diego
; STATE: California

COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-410-804-13

Query Match 53.1%; Score 18.6; DB 1; Length 27;
Best local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcgtggaga 35
||| |
Db 1 GGAATTCATGGCGCAGCTGGAGA 25

RESULT 13
US-08-607-269-8
Sequence 8, Application US/08607269
Patent No. 5702897
GENERAL INFORMATION:
APPLICANT: Reed, John C.
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TITLE OF INVENTION: Interaction of Proteins Involved in a
CELL DEATH PATHWAY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-607-269-8

Query Match 53.1%; Score 18.6; DB 1; Length 27;
Best local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcgtggaga 35
||| |
Db 1 GGAATTCATGGCGCAGCTGGAGA 25

RESULT 14
US-08-259-514-13
Sequence 13, Application US/08259514
Patent No. 5747245
GENERAL INFORMATION:
APPLICANT: Reed, John C.
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,514
FILING DATE: 14-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9954
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-259-514-13

Query Match 53.1%; Score 18.6; DB 1; Length 27;
Best local Similarity 84.0%; Pred. No. 16;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcgtggaga 35
||| |
Db 1 GGAATTCATGGCGCAGCTGGAGA 25

RESULT 15

US-08-858-311-13
 ; Sequence 13, Application US/08858311
 ; Patent No. 5876939
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, John C.
 ; APPLICANT: Sato, Takaaki
 ; TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Cathryn Campbell
 ; STREET: 4370 La Jolla Village Drive, Ste 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/858,311
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/410,804
 ; FILING DATE: 27-MAR-1995
 ; APPLICATION NUMBER: US 08/259,514
 ; FILING DATE: 14-JUN-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LJ 1389
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 27 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: CDNA
 ; US-08-858-311-13

Query Match 53.18; Score 18.6; DB 2; Length 27;
 Best Local Similarity 84.08; Pred. No. 16;
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 gggaagatgagcagcgtggaga 35
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 DB 1 GGAAATCATGGCGACGCTGGAGA 25

Search completed: June 28, 2002, 22:16:39
 Job time: 8265 sec

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C	3	20	100.0	33	6	AR052606	AR052606 Sequence
C	4	20	100.0	33	6	196085	196085 Sequence 4
C	5	13.6	68.0	51	6	AX116165	AX116165 Sequence
C	6	13.4	67.0	49	9	HSHLX1D2	X96916 H.sapiens H
C	7	13.2	66.0	31	6	AR098300	AR098300 Sequence
C	8	13.2	66.0	40	10	MUSRIBBF	L35085 Mus musculus
C	9	13.2	66.0	51	6	AX156665	AX156665 Sequence
C	10	13	65.0	22	6	AR068325	AR068325 Sequence
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C	22	12.6	63.0	75	6	AR035203	AR035203 Sequence
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C	26	12.2	61.0	20	6	AR137423	AR137423 Sequence
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C	29	12.2	61.0	21	6	AX113936	AX113936 Sequence
C	30	12.2	61.0	24	6	AX289570	AX289570 Sequence
C	31	12.2	61.0	24	6	169149	169149 Sequence 41
C	32	12.2	61.0	25	6	AX128282	AX128282 Sequence
C	33	12.2	61.0	34	6	AX037019	AX037019 Sequence
C	34	12.2	61.0	42	6	AX328775	AX328775 Sequence
C	35	12.2	61.0	50	6	AR032713	AR032713 Sequence
C	36	12.2	61.0	50	6	129453	129453 Sequence 32
C	37	12.2	61.0	50	6	191127	191127 Sequence 32
C	38	12.2	61.0	51	6	AX204060	AX204060 Sequence
C	39	12.2	61.0	57	9	HSDFCRV13	L27191 H.sapiens r
C	40	12.2	61.0	57	9	AF084011	AF084011 Homo sapi
C	41	12.2	61.0	57	9	AF084014	AF084014 Homo sapi
C	42	12.2	61.0	57	9	AF084019	AF084019 Homo sapi
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Db 1 GATGCACCTACCAGCCTCC 20

RESULT 2
196084
LOCUS Sequence 3 from patent US 5734033.
DEFINITION 196084
ACCESSION 196084.1 GI:3940554
VERSION
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 20)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 3 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 10 c 3 g 3 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatgcacctaccagctcc 20
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Db 1 GATGCACCTACCAGCCTCC 20

RESULT 3
AR052606/c
LOCUS AR052606 33 bp. DNA
DEFINITION Sequence 4 from patent US 5831066.
ACCESSION AR052606
VERSION AR052606.1 GI:5975970
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 4 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 5 a 5 c 16 g 7 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatgcacctaccagctcc 20
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Db 29 GATGCACCTACCAGCCTCC 10

RESULT 4
196085/c
LOCUS Sequence 4 from patent US 5734033.
DEFINITION 196085
ACCESSION 196085.1 GI:3940555
VERSION

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 33)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 4 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..33
/organism="unknown"

BASE COUNT 5 a 5 c 16 g 7 t
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Query Match 100.0%; Score 20; DB 6; Length 33;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gatgcacctaccagctcc 20
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Db 29 GATGCACCTACCAGCCTCC 10

RESULT 5
AX116165/c
LOCUS AX116165 51 bp. DNA
DEFINITION Sequence 1288 from Patent W00129262.
ACCESSION AX116165
VERSION AX116165.1 GI:14033107
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1288 26-APR-2001;
FEATURES Location/Qualifiers
source 1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 9 a 11 c 24 g 7 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 2.1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 49 GATGCCCTCCCGCCTCC 30

RESULT 6
HSHLX1D2/c
LOCUS HSHLX1D2 46 bp. DNA
DEFINITION H.sapiens Hlx-1 gene, donor second intron.
ACCESSION X96916
VERSION X96916.1 GI:1770446
KEYWORDS Hlx-1 gene; LIM 1 protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 46)
AUTHORS Bozzl,F., Bertuzzi,S., Strina,D., Giannetto,C., Vezzoni,P. and
Villa,A.
TITLE The exon-intron structure of human LHX1 gene
JOURNAL Biochem. Biophys. Res. Commun. 229 (2), 494-497 (1996)

Mon Jul 1 08:40:54 2002

us-09-709-170a-3.sz1m75.ige

MEDLINE 97127430
2 (bases 1 to 46)
REFERENCE Bozzi F, Potter M, and Janz S.
AUTHORS Direct Submission
TITLE Submitted (22-MAR-1996) F. Bozzi, ITBA - CNR, via Ampere 56, 20131
JOURNAL Milan, ITALY
Location/Qualifiers
FEATURES
source
1. /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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/map="p12"
1. /gene="Hlx-1"
46
/note="donor second intron"
misc-feature /product="LIM 1 protein" 9 t
12 c

BASE COUNT 6 a 67.0%; Score 13.4; DB 9; Length 46;
ORIGIN 67.0%; Pred. No. 2.7e+04; Indels 1; Gaps 0;
Query Match 93.3%; 0; Mismatches 1;
Best Local Similarity 93.3%; 0; Mismatches 1;
Matches 14: Conservative

QY 3 tgcacctaccagctcc 17
32 tgcacctaccagctcc 18
Db 32 tgcacctaccagctcc 18
31 bp DNA
PAT 14-FEB-2001

RESULT 7
AR098300/c AR098300 13 from patent US 6074872.
LOCUS Sequence
DEFINITION AR098300.1 GI:12807557
ACCESSION AR098300.1
VERSION
KEYWORDS
ORGANISM Unknown.
SOURCE Unclassified.
REFERENCE 1 (bases 1 to 31)
AUTHORS Sutoh T, J. Gregor and de laecea L.
Cottislatin: nucleic acids that encode these neuropeptides
TITLE Patent: US 6074872-A 13 JUN-2000;
JOURNAL Location/Qualifiers
FEATURES
source
1. /organism="unknown"
4 c 13 g 6 t

BASE COUNT 8 a 66.0%; Score 13.2; DB 6; Length 31;
ORIGIN 66.0%; Pred. No. 3.6e+04; Indels 3; Gaps 0;
Query Match 83.3%; 0; Mismatches 3;
Best Local Similarity 83.3%; 0; Mismatches 3;
Matches 15: Conservative

QY 3 tgcacctaccagctcc 20
30 tgcacctaccagctcc 13
40 bp DNA
linear ROD 12-AUG-1994
PAT 29-SEP-1994

RESULT 8
MUSTRRBF MUSTRRBF 40 bp
LOCUS Mus musculus (individual isolate primary plasmacytoma 4122, strain
DEFINITION U55085.1 GI:529452
ACCESSION U55085.1 GI:529452
VERSION U55085.1 GI:529452
KEYWORDS Mus musculus (individual isolate primary plasmacytoma 4122, strain
SOURCE Mus musculus (individual isolate primary plasmacytoma 4122, strain
ORGANISM Mus musculus (individual isolate primary plasmacytoma 4122, strain
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 40)
AUTHORS Bozzi F, Potter M, and Janz S.
TITLE Differences in the molecular structure of c-myc activating
Recombinations in murine plasmacytomas and precursor cells
Proc. Natl. Acad. Sci. U.S.A. (1994) 10 press
JOURNAL Location/Qualifiers
FEATURES
source
1. /organism="Mus musculus"
40
/strain="BALB/c AnP1"
/isolate="primary plasmacytoma 4122"
/db_xref="taxon:10090"
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20
/note="translocation breakpoint t(12:15) on the c-myc
activating chr 12+
activating chr 12+
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9 a 17 c

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ORIGIN 66.0%; Pred. No. 3.5e+04; Indels 3; Gaps 0;
Query Match 83.3%; 0; Mismatches 3;
Best Local Similarity 83.3%; 0; Mismatches 3;
Matches 15: Conservative

QY 3 tgcacctaccagctcc 20
1 tgcacctaccagctcc 18
51 bp DNA
linear PAT 22-JUN-2001

RESULT 9
AX165665 AX165665 860 from patent WO0138586.
LOCUS Sequence
DEFINITION AX165665.1 GI:14546494
ACCESSION AX165665.1
VERSION
KEYWORDS
ORGANISM human.
SOURCE Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Differences in the molecular structure of c-myc activating
Recombinations in murine plasmacytomas and precursor cells
Proc. Natl. Acad. Sci. U.S.A. (1994) 10 press
JOURNAL Location/Qualifiers
FEATURES
source
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51
/db_xref="taxon:9606"
/note="single nucleotide polymorphism
Accession number c943981852"
26
Accession number c943981852"
10 t
4 a 24 c 13 g

BASE COUNT 4 a 66.0%; Score 13.2; DB 6; Length 51;
ORIGIN 66.0%; Pred. No. 3.4e+04; Indels 3; Gaps 0;
Query Match 83.3%; 0; Mismatches 3;
Best Local Similarity 83.3%; 0; Mismatches 3;
Matches 15: Conservative

QY 3 tgcacctaccagctcc 20
8 tgcacctaccagctcc 25
22 bp DNA
linear PAT 29-SEP-1999

RESULT 10
AR068325 AR068325 10 from patent US 5853977.
LOCUS Sequence
DEFINITION AR068325.1 GI:6000532
ACCESSION AR068325.1
VERSION

KEYWORDS
SOURCE Unknown
ORGANISM Unknown
REFERENCE Unclassified
AUTHORS 1 (bases 1 to 22)
TITLE Dille, B., Tan, X., Lundell, D., Lund, C.A., Tan, J.C. and Zavadny, P.J.
JOURNAL Mammalian TMR-Alpha Convertases
FEATURES Patent: US 5853977-A, 10-29-DEC-1998;
source location/Qualifiers
BASE COUNT 4 a 12 c 3 g 3 t
ORIGIN /organism="unknown"

Query Match
Best Local Similarity 65.0%; Score 13; DB 6; Length 22;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 cctaccagcctc 19
Db 8 cctaccagcctc 20

RESULT 11
LOCUS E07533/c
DEFINITION Oligonucleotide primer encoding the amino acid sequence included in
ACCESION E07533
VERSION E07533.1 GI:2175668
KEYWORDS JP 1994141863-A/2.
SOURCE ORGANISM unidentified.
REFERENCE 1 (bases 1 to 30)
AUTHORS Morita, T. and Matsushiro, A.
TITLE MURINE GENE PARTIAL CLONING IN HOMOLOGOUS RECOMBINING REACTION
JOURNAL MORITA, JP 1994141863-A 2 24-MAY-1994;
COMMENT OS None
OC Artificial sequences.
FN JP 1994141863-A/2
PD 24-MAY-1994
PI 10-MAY-1994
PC MORITA TAKASHI, MATSUSHIRO AIZO
CC C12N15/12, C12N1/19//C12Q1/68;
CC strandness: Single;
CC topology: Linear;
FH key
FT source location/Qualifiers
FT 1.30
/organism="Artificial sequences",
/db_xref="taxon:32644"

BASE COUNT 6 a 5 c 7 g 5 t 7 others
ORIGIN /db_xref="taxon:32644"

Query Match
Best Local Similarity 65.0%; Score 13; DB 6; Length 30;
Matches 13; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 gctgacctaccagcctc 20
Db 22 gctgacctaccagcctc 20
RESULT 12
LOCUS AX092953
AX092953 31 bp DNA linear PAT 30-MAR-2001

DEFINITION Sequence 12 from Patent W00118225.
ACCESSION AX092953
VERSION AX092953.1 GI:13509438
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 31)
AUTHORS Zhang, N.N.
TITLE Targeting constructs and transgenic animals produced therewith
JOURNAL Patent: WO 0118225-A 12 13-MAR-2001;
Xenogen Corporation (US)
FEATURES location/Qualifiers
source 1.31
/organism="synthetic construct",
/db_xref="taxon:32630"
BASE COUNT 9 a 10 c 9 g 3 t
ORIGIN /note="primer VNIP"

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Best Local Similarity 64.0%; Score 12.8; DB 6; Length 31;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 atgcacctaccagc 17
Db 4 atgcacctaccagc 17

RESULT 13
LOCUS AX167323
DEFINITION Sequence 12 from Patent W00144460.
ACCESSION AX167323
VERSION AX167323.1 GI:1456762
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 31)
AUTHORS Contag, P.R., Purcell, O.A.X. and Zhang, N.X.
TITLE Methods and compositions for screening for angiogenesis modulating
JOURNAL Patent: WO 0144460-A 12 21-JUN-2001;
Xenogen Corporation (US)
FEATURES location/Qualifiers
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/organism="synthetic construct",
/db_xref="taxon:32630"
BASE COUNT 9 a 10 c 9 g 3 t
ORIGIN /note="primer VNIP"

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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 atgcacctaccagc 17
Db 4 atgcacctaccagc 17
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LOCUS AR088563/c
DEFINITION Sequence 12 from Patent US 5989899.
ACCESSION AR088563
VERSION AR088563.1 GI:10015327
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 39)

AUTHORS Bower, B.S., Clarkson, K.A., Larenas, E.A. and Ward, M.

TITLE Oversized cellulase compositions for use in detergent compositions

and in the treatment of textiles

Patent: US 5989899-A 12 23-NOV-1999;

JOURNAL Location/Qualifiers

FEATURES 1..39

source /organism="unknown"

BASE COUNT 6 a 9 c 15 g 9 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 39;

Best Local Similarity 87.5%; Pred. No. 5.8e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 gcacctaccagctc 19

I | | | | | | | | | |

Db 36 GGACCTACCAGCTCTC 21

RESULT 15

AR088564

LOCUS AR088564 39 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 13 from patent US 5989899.

ACCESSION AR088564

VERSION AR088564.1 GI:10015328

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 39)

AUTHORS Bower, B.S., Clarkson, K.A., Larenas, E.A. and Ward, M.

TITLE Oversized cellulase compositions for use in detergent compositions

and in the treatment of textiles

Patent: US 5989899-A 12 23-NOV-1999;

JOURNAL Location/Qualifiers

FEATURES 1..39

source /organism="unknown"

BASE COUNT 9 a 15 c 9 g 6 t

ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 39;

Best Local Similarity 87.5%; Pred. No. 5.8e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4 GGACCTACCAGCTCTC 19

Search completed: June 28, 2002, 22:10:50
Job time: 8341 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:02 ; Search time 1381.16 seconds

(without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170A-3

Perfect score: 20

Sequence: 1 gatgcacctaccagcctcc 20

Scoring table: IDENTITY_NUC

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Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	19	AAV19654
3	20	100.0	33	AAQ86646
4	14.2	71.0	26	AAV19654
5	14.2	71.0	21	AAZ57423
6	13.8	69.0	47	AAZ68500
7	13.6	68.0	21	AAZ68807
8	13.2	66.0	51	AAH38492
9	13.2	66.0	31	AAV09157
			41	AAI68122

10	13.2	66.0	41	AAI68123	Human growth hormo
11	13.2	66.0	51	AAI27169	Human SNP oligonuc
12	13.2	66.0	51	AAI31174	Human SNP oligonuc
13	13.2	66.0	51	AAI32505	Human SNP oligonuc
14	13.2	66.0	51	AAI32607	Human SNP oligonuc
15	13.2	66.0	51	AAI33975	Human SNP oligonuc
16	13.2	66.0	51	ABL00869	Human amino acid c
17	13.2	65.0	22	AAV20581	Human MT-MMP2 PCR
18	13	65.0	22	AAV73937	Human TNF-alpha co
19	13	65.0	30	AAO64086	Rad51 primer. Syn
20	12.8	64.0	20	AAO60942	Interleukin 10 sho
21	12.8	64.0	22	AAV41635	Nucleotide sequenc
22	12.8	64.0	22	AAV69953	PCR primer used to
23	12.8	64.0	31	AAH24926	PCR primer for mur
24	12.8	64.0	31	AAO1053	Mouse 3'end vitron
25	12.8	64.0	31	AAO22497	Mouse vitronectin
26	12.8	64.0	39	AAV44776	PCR primer for end
27	12.8	64.0	39	AAV44777	PCR primer for end
28	12.8	64.0	50	AAI33644	Human SNP oligonuc
29	12.8	64.0	51	AAH90214	Human clone c94402
30	12.8	64.0	72	AAO91280	Exo-cellulohydroly
31	12.6	63.0	49	AAI74185	Human silent SNP c
32	12.6	63.0	51	AAI31094	Human SNP oligonuc
33	12.6	63.0	51	AAH38988	Human SNP flanking
34	12.6	63.0	75	AAO30885	Primer 312-59. SY
35	12.6	63.0	75	AAO30886	Primer 312-60. SY
36	12.4	62.0	17	AAV95263	Human c-fos target
37	12.4	62.0	20	AB196525	Capture oligonucle
38	12.4	62.0	24	AAI516083	Hybridised tagged
39	12.4	62.0	24	AB189620	Capture oligonucle
40	12.4	62.0	24	AB189621	Capture oligonucle
41	12.4	62.0	27	AAI33844	HBV probe G. Synt
42	12.4	62.0	30	AAH80762	Probe for detectio
43	12.4	62.0	30	AAH22223	Probe for HIV-1 VI
44	12.4	62.0	47	AAZ66889	Human map-related
45	12.2	61.0	20	AAZ95165	Primary forward PC

ALIGNMENTS

RESULT 1	
AAV19653	
ID AAV19653 standard; DNA; 20 BP.	
XX AAV19653;	
AC	
XX	
DT 12-JUN-1998 (first entry)	
XX	
DE Human bcl-2 antisense oligonucleotide 2.	
XX	
KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;	
KW cancer; ss.	
XX	
OS Synthetic.	
OS Homo sapiens.	
XX	
PN US5734033-A.	
XX	
PD 31-MAR-1998.	
XX	
PF 24-MAR-1994; 94US-0288692.	
XX	
PR 21-FEB-1992; 92US-0840716.	
XX	
PR 22-DEC-1988; 88US-0288692.	
XX	
PR 24-MAR-1994; 94US-0217082.	
XX	
PA (TYPE-) UNIV PENNSYLVANIA.	
XX	
PI Reed J;	
XX	
DR WPI; 1998-229881/20.	

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Claim 6; Columns 3-4; 21pp; English.

CC This antisense oligonucleotide is complementary to the splice donor
CC site of the human bcl-2 mRNA. The Bcl-2 antisense oligonucleotides are
CC phosphorothioate derivatives and can straddle strategic sites such as the
CC translation initiation site, donor and acceptor splicing sites, or sites
CC for transportation or degradation. Blocking translation at such strategic
CC sites prevents the formation of a functional bcl-2 gene product. These
CC oligonucleotides may be used for treating cancers associated with high
CC levels of bcl-2 gene expression, especially lymphomas and some
CC leukaemias.

XX Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gatgcactaccagctcc 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 gatgcactaccagctcc 20

RESULT 2

AA086646/c
ID AA086646 standard; DNA; 33 BP.

XX AA086646;

XX 27-SEP-1995 (first entry)

DE Bcl-2 splice donor site.

XX Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;

XX ss.

OS Synthetic.

XX WO9508350-A.

XX 30-MAR-1995.

XX 20-SEP-1994; 94WO-US10725.

XX 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

XX WPI; 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PS Disclosure; Page 13; 108pp; English.

CC The antisense oligonucleotide SD-AS (AA086645) is complementary to a
CC portion of the splice donor site of the pre-mRNA coding strand of the
CC human bcl-2 gene. It reduces the expression of bcl-2 gene product,
CC thereby inducing programmed cell death of certain cancer cells. The
CC corresp. bcl-2 sense splice donor site region was synthesized for use
CC as a control.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gatgcactaccagctcc 20
| | | | | | | | | | | | | | | | | | | | | |
Db 29 GATGCACCTACCCAGCCTCC 10

RESULT 3

AAV19654/c
ID AAV19654 standard; DNA; 33 BP.

XX AAV19654;

XX 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 2.

XX Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5734033-A.

XX 31-MAR-1998.

XX 24-MAR-1994; 94US-0288692.

XX 21-FEB-1992; 92US-0840716.

XX 22-DEC-1988; 88US-0288692.

XX 24-MAR-1994; 94US-0217082.

XX (TYPE-) UNIV PENNSYLVANIA.

PI Reed J;

XX WPI; 1998-229881/20.

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

PS Disclosure; Columns 3-4; 21pp; English.

CC This is a human bcl-2 oligonucleotide based on which an antisense
CC oligonucleotide complementary to the splice donor site of the human
CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
CC strategic sites such as the translation initiation site, donor and
CC acceptor splicing sites, or sites for transportation or degradation.
CC Blocking translation at such strategic sites prevents the formation of a
CC functional bcl-2 gene product. These oligonucleotides may be used for
CC treating cancers associated with high levels of bcl-2 gene expression,
CC especially lymphomas and some leukaemias.

XX Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gatgcactaccagctcc 20
| | | | | | | | | | | | | | | | | | | | | |
Db 29 GATGCACCTACCCAGCCTCC 10

RESULT 4

AAZ57423
ID AAZ57423 standard; DNA; 26 BP.

XX AAZ57423;

DT 07-APR-2000 (first entry)
XX
DE Oligonucleotide PCR primer pair #3 primer #1.
XX
KW PCR primer: Zaocys dhumnade; Tortoise plastron; Oviductus ranae;
KW discrimination: black snake; forest frog; oil; reagent box;
KW medicinal; ss.
XX
OS Synthetic.
XX
PN CN1232085-A.
XX
PD 20-OCT-1999.
XX
PF 31-MAR-1999; 99CN-0114133.
XX
PR 31-MAR-1999; 99CN-0114133.
XX
PA (UYNA-) UNIV NANTING.
XX
PI Wang Y, Zhou K, Liu Z;
XX
DR WPI: 2000-098492/09.
XX
PT Polymerase chain reaction (PCR) determining primer for Zaocys dhumnade,
PT Tortoise plastron and Oviductus ranae -
XX
PS Claim 1; Page 1; 4pp; Chinese.
XX
CC The present invention describes a special DNA sequence which can be used
CC to synthesise three pairs of high-specificity primers useful for
CC discriminating if black snake, tortoise plastron and forest frog oil are
CC true or false by simple polymerase chain reaction (PCR) of their DNA.
CC AA27419 to AA27424 represent specifically claimed primers from the
CC present invention. The primers can be used to make a reagent box for
CC discriminating medicinal materials with high speed and quality.
XX
SQ Sequence 26 BP; 6 A; 12 C; 1 G; 7 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 26;
Best Local Similarity 84.2%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gatgcacctaccagcctc 19
||| ||||| ||| |||||
DB 4 gatcactaaccatcctc 22

RESULT 5
AA268500
ID AA268500 standard; DNA: 47 BP.
XX
AC AA268500;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:2847.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(24,C)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN W09954500-A2.
XX

PD 28-OCT-1999.
XX
PF 21-APR-1999; 99MO-TR00822.
XX
XX 21-APR-1998; 98US-0082614.
PR 23-NOV-1998; 98US-0109732.
XX
XX (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel diallelic markers used to construct a high density disequilibrium
PT map of the human genome -
XX
PS Claim 3; Page 837; 2745pp; English.
XX
CC AA26564 to AA269578 represent human diallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the diallelic markers. The diallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 16 A; 13 C; 10 G; 8 T; 0 other;

Query Match 71.0%; Score 14.2; DB 21; Length 47;
Best Local Similarity 84.2%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gatgcacctaccagcctc 19
||||| ||||| ||||| |||||
DB 24 gatgcactaaccagccccc 42

RESULT 6
AA268807/c
ID AA268807 standard; DNA: 47 BP.
XX
AC AA268807;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related diallelic marker SEQ ID NO:3160.
XX
KW Human genome; diallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Variation replace(24,G)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN W09954500-A2.
XX
PD 28-OCT-1999.
XX

PA (SCRI) SCRIPPS RES INST.
 XX De Lecea L, Henriksen SJ, Sigsgaard GR, Sutcliffe JG;
 XX WPI; 1998-008886/01.
 DR
 XX
 PT New cortistatin peptide(s) - used to modulate sleep, detect
 PT mutation(s) and screen for drugs
 XX
 PS Claim 7; Page 107; 128pp; English.
 XX
 CC This is a 5' PCR primer used in the amplification of the novel
 CC prepro-cortistatin protein. Cleavage of the protein leads to the
 CC formation of pro-cortistatin, which is processed to produce the mature
 CC cortistatin protein referred to as rat cortistatin-29, and cortistatin-14.
 CC The purified cortistatin, and its agonists, are used to induce sleep
 CC while its receptor antagonists (particularly antihistamines) is used to
 CC inhibit sleep. Although cortistatin is structurally similar to
 CC somatostatin, it is able to depress neuronal electrical activity, induce
 CC low frequency waves in the cerebral cortex, antagonise acetylcholine and
 CC therefore enhance slow-wave sleep. The antibodies, and oligonucleotide
 CC primers, are used in usual immunoassays and hybridisation/amplification
 CC assays to detect or quantify cortistatin (including that administered
 CC therapeutically) or its nucleic acid. Oligonucleotides, e.g. antisense
 CC molecules, are used in vivo to alter cortistatin gene expression.
 CC Detection of a mutation in the cortistatin gene may provide diagnosis of
 CC sleep-related or neuronal depression-related disorders or diseases of
 CC the brain.
 XX
 SQ Sequence 31 BP; 8 A; 4 C; 13 G; 6 T; 0 other;
 XX
 Query Match 66.0%; Score 13.2; DB 19; Length 31;
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 3 tgcacctaccacgacctcc 20
 ||||| ||||| |||||
 Db 30 TGCAGCCACCCATCCTCC 13
 XX
 RESULT 9
 AA168122/c
 ID AA168122 standard; DNA; 41 BP.
 XX
 AC AA168122;
 XX
 DT 13-DEC-2001 (first entry)
 XX
 DE Human growth hormone family protein 9 probe 1.
 XX
 DE Human growth hormone family protein 9; cytostatic; virucidal; HIV;
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
 KW human immunodeficiency virus; infection; immunological disease;
 KW embryonic developmental disorder; growth disturbance;
 KW developmental disturbance; pregnancy abnormality; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200170809-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-CN00214.
 XX
 PR 07-MAR-2000; 2000CN-0111926.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-611485/70.
 XX

PT New protein 9 of growth hormone family and encoded polynucleotide,
 PT applicable in diagnosis and treatment of e.g. developmental disorders,
 PT tumour, haemopathy, human immunodeficiency virus infection, immunological
 PT diseases and inflammation
 XX
 PS Example 6; Page 15; 34pp; Chinese.
 XX
 CC The invention relates to human growth hormone family protein 9 with
 CC cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic
 CC activity. The polypeptide and encoded polynucleotide are applicable in
 CC diagnosis and treatment of malignant tumour, haemopathy, human
 CC immunodeficiency virus infection, immunological diseases and various
 CC inflammations, embryonic developmental disorders, growth disturbance,
 CC developmental disturbance and pregnancy abnormality. The present sequence
 CC is that of a probe, useful to the invention.
 XX
 SQ Sequence 41 BP; 9 A; 6 C; 20 G; 6 T; 0 other;
 XX
 Query Match 66.0%; Score 13.2; DB 22; Length 41;
 Best Local Similarity 83.3%; Pred. No. 4.6e+03;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 QY 3 tgcacctaccacgacctcc 20
 ||||| ||||| |||||
 Db 29 TGCACCTAGCCACCTCC 12
 XX
 RESULT 10
 AA168123/c
 ID AA168123 standard; DNA; 41 BP.
 XX
 AC AA168123;
 XX
 DT 13-DEC-2001 (first entry)
 XX
 DE Human growth hormone family protein 9 probe 2.
 XX
 DE Human growth hormone family protein 9; cytostatic; virucidal; HIV;
 KW immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
 KW human immunodeficiency virus; infection; immunological disease;
 KW embryonic developmental disorder; growth disturbance;
 KW developmental disturbance; pregnancy abnormality; probe; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200170809-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-CN00214.
 XX
 PR 07-MAR-2000; 2000CN-0111926.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-611485/70.
 XX
 PD 27-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-CN00214.
 XX
 PR 07-MAR-2000; 2000CN-0111926.
 XX
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2001-611485/70.
 XX

CC developmental disturbance and pregnancy abnormality. The present sequence
CC is that of a probe, useful to the invention.
XX
SQ Sequence 41 BP; 9 A; 6 C; 20 G; 6 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 41;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 tgcacctaccagctcc 20
||||||| 1111111
DB 29 tgcacctaccagctcc 12

RESULT 11

AAL27169/c
ID AAL27169 standard; DNA; 51 BP.

XX AAL27169;

DT 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #377.

DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.

OS Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections -

XX Claim 1; Page 1500; 4143pp; English.

PS The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms.

XX Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atgcactaccagctcc 19
||||| 11111111111
DB 24 atgcactaccagctcc 7

RESULT 12

AAL31174
ID AAL31174 standard; DNA; 51 BP.

XX AAL31174;

DT 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #4382.

DE Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amyase; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.

OS Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g.
XX cancer, autoimmune diseases and infections -

XX Claim 1; Page 2645; 4143pp; English.

PS The present invention relates to oligonucleotides encoding polymorphic
XX variants of proteins related to amylases, amyloid proteins, angiotensin,
XX apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX histones, kinases, colony stimulating factors, complement related
XX proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX G-protein coupled receptors and thioesterases. The present sequence is
XX one such oligonucleotide. The oligonucleotides and the peptides encoded
XX by them may be used in the prevention, diagnosis and treatment of
XX diseases associated with inappropriate expression of the proteins listed
XX above. Disorders that may be prevented, diagnosed and/or treated include
XX multifactorial diseases with a genetic component, such as autoimmune
XX diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX leukaemia), diseases of the nervous system and an infection of pathogenic
XX organisms.

Sequence 51 BP; 9 A; 17 C; 13 G; 12 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 atgcacctaccagcctc 19
| ||||| |||||
Db 5 aggcagcctccagcctc 22

RESULT 13

AAL32505/c

ID AAL32505 standard; DNA; 51 BP.

AC AAL32505;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #5713.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3032; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

SQ Sequence 51 BP; 8 A; 9 C; 18 G; 16 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 atgcacctaccagcctc 19
| ||||| |||||
Db 51 ATCCAGCAGCTCAGCCTC 34

RESULT 14

AAL32607/c

ID AAL32607 standard; DNA; 51 BP.

AC AAL32607;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #5815.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PR 27-DEC-2000; 2000US-0173419.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections -

PS Claim 1; Page 3059; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

SQ Sequence 51 BP; 8 A; 11 C; 23 G; 9 T; 0 other;

Query Match 66.0%; Score 13.2; DB 22; Length 51;
Best Local Similarity 83.3%; Pred. No. 4.7e+03;

	Matches	15; Conservative	0;	Mismatches	3;	Indels	0;	Gaps	0;
QY	2	atgacacctaccagcctc	19						
Db	47	ATGCCCATGCCCAAGCCTC	30						

QY	3	tgcacctaccacgctcc	20
Db	2	ttcacgttcccagcctcc	19

```
Search completed: June 28, 2002, 22:40:04
Job time: 8080 sec
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RESULT	15
AL33975	
ID	AL33975 standard; DNA; 51 BP.
XX	
AC	AL33975;
XX	
DF	24-JAN-2002 (first entry)
XX	
DE	Human SNP oligonucleotide #7183

KM Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KM neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KM cyclin D polymerase; oncogene; histone; kinase; colony stimulating factor
 KM complement related protein; cytochrome; kinase; cytokine; interferon;
 KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KM multifactorial disease; autoimmune disease; infection;
 KM nervous system disease; ss.

Homo sapiens.

WO200147944-A2.

05-JUL-2001.

28-DEC-2000; 2000WO-US35498.

28-DEC-1999; 99US-0173419.

27-DEC-2000; 2000US-0173419.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2001-465210/50.

Polymorphic nucleic acids encoding e.g. amyloses, cyclins, polymerases oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -

Claim 1; Page 3448; 4143pp; English.

The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amylolipid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukemia), diseases of the nervous system and an infection of pathogenic organisms.

50 Sequence 51 BP; 8 A; 19 C; 12 G; 12 T; 0 other;

Query Match	66.0%;	Score 13.2;	DB 22;	Length 51;
Best Local Similarity	83.3%;	Pred. No. 4.7e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Mon Jul 1 08:40:54 2002

us-09-709-170a-3.szlm75.rng

Search time about	alignments)	updates/sec
334.0		
311		

June 28, 2007

Sequence:	Score:	Title:
1 gatgcacctacc...	20	perfect score:

Searched:

Database :

pred. not greater than O-
score greater by analysts O-
and is derived by analysts O-
SUMMARIES

Description

Result No.	Score	Query Length	DB	ID	Sequence
1	20	100.0	20	1	Sequence 3, Appl1
2	20	100.0	20	1	Sequence 3, Appl1
3	20	100.0	20	1	Sequence 3, Appl1
4	20	100.0	20	1	Sequence 3, Appl1
5	20	100.0	20	1	Sequence 3, Appl1
6	20	100.0	20	1	Sequence 3, Appl1
7	20	100.0	20	1	Sequence 3, Appl1
8	20	100.0	20	1	Sequence 3, Appl1
9	20	100.0	20	1	Sequence 3, Appl1
10	20	100.0	20	1	Sequence 3, Appl1
11	20	100.0	20	1	Sequence 3, Appl1
12	20	100.0	20	1	Sequence 3, Appl1
13	20	100.0	20	1	Sequence 3, Appl1
14	20	100.0	20	1	Sequence 3, Appl1
15	20	100.0	20	1	Sequence 3, Appl1
16	20	100.0	20	1	Sequence 3, Appl1
17	20	100.0	20	1	Sequence 3, Appl1
18	20	100.0	20	1	Sequence 3, Appl1
19	20	100.0	20	1	Sequence 3, Appl1
20	20	100.0	20	1	Sequence 3, Appl1
21	20	100.0	20	1	Sequence 3, Appl1
22	20	100.0	20	1	Sequence 3, Appl1
23	20	100.0	20	1	Sequence 3, Appl1
24	20	100.0	20	1	Sequence 3, Appl1
25	20	100.0	20	1	Sequence 3, Appl1
26	20	100.0	20	1	Sequence 3, Appl1
27	20	100.0	20	1	Sequence 3, Appl1

[illegible]

RESULT 1
US-08-217-082A-3 Application US/08217082A
Sequence 3, 5749103
Patent No. 5749103
GENERAL INFORMATION: John
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: OBLOM, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
ADDRESS: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/217,082A
APPLICATION NUMBER: US61934
FILING DATE: 24-MAR-1994
CLASSIFICATION DATA: US 07/840,716
PRIORITY APPLICATION NUMBER: 21-FEB-1992
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA: US 07/288,692
APPLICATION NUMBER: 22-DIS-C-1988
FILING DATE: 22-DIS-C-1988
ATTORNEY/AGENT INFORMATION: AGNEW D.
NAME: FORTNEY, Agnew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET INFORMATION: 3335-067-55 FWC
TELEPHONE: (408) 436-2070
TELEFAX: (408) ID NO.: 3
INFORMATION FOR SPONSORS: 436-2075
SEQUENCE CHARACTERISTICS: 436-2070
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: linear
TOPOLOGY: other nucleic acid
MOLECULE TYPE: synthetic DNA
DESCRIPTION: YES
ANTI-SENSE: YES

US-08-217-082A-3

Mon Jul 1 08:40:54 2002

us-09-709-1704-3.s21m75.fn1

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 gatgcacctaccagctcc 20
DB 1 gatgcacctaccagctcc 20

RESULT 2
US-08-465-485A-3

Sequence 3, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS: 29
ADDRESS: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 514
CLASSIFICATION: US/08/465,485A
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 514
PRIORITY APPLICATION DATE: 20-SEP-1993
PRIORITY APPLICATION NUMBER: US 08/124,256
PRIORITY APPLICATION DATE: 21-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcacctaccagctcc 20
DB 1 gatgcacctaccagctcc 20

RESULT 3
US-09-080-285-3

Query Match
Best Local Similarity 100.0%; Score 20; DB 3; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcacctaccagctcc 20
DB 1 gatgcacctaccagctcc 20

RESULT 4
US-08-217-082A-4/c

Sequence 4, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: 17
ADDRESS: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 514
CLASSIFICATION: US/09/080,285
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 514
PRIORITY APPLICATION DATE: 20-SEP-1993
PRIORITY APPLICATION NUMBER: US 08/124,256
PRIORITY APPLICATION DATE: 21-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES

ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-4

Query Match 100.0%; Score 20; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcactaccagctcc 20
|||||
Db 29 GATGCACCTACCGACCTCC 10

RESULT 5
US-08-465-485A-4/C
Sequence 4, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-4

Query Match 100.0%; Score 20; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gatgcactaccagctcc 20
|||||
Db 29 GATGCACCTACCGACCTCC 10

RESULT 6
US-09-080-285-4/C
Sequence 4, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-4

Query Match 100.0%; Score 20; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gatgcacctaccagctcc 20
|||||
Db 29 GATGCACCTACCAGCCTCC 10

RESULT 7
US-08-648-322-13/C
Sequence 13, Application US/08648322
Patent No. 6074872
GENERAL INFORMATION:
APPLICANT: Sutcliffe, Gregor J.
APPLICANT: de Lecea, Luis
TITLE OF INVENTION: CORTISTATIN: NEUROPEPTIDES,
TITLE OF INVENTION: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. 6074872th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,322
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 519.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 554-2937
TELEFAX: (619) 554-6312
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-648-322-13

Query Match 66.0%; Score 13.2; DB 3; Length 31;

Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 3 tgcacctaccagctcc 20
|||||
Db 30 TGCAGCCACCACCTCC 13

RESULT 8
US-08-889-909A-10
Sequence 10, Application US/08889909A
Patent No. 5853977
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Fan, Xuedong
APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles
APPLICANT: Tan, Jimmy
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Mammalian TNF-a Convertases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,909A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/021,710
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dulak, No. 5853977man C.
REGISTRATION NUMBER: 31,608
REFERENCE/DOCKET NUMBER: JB0601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 2906
TELEFAX: 908 298 5388
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-889-909A-10

Query Match 65.0%; Score 13; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 cctaccagctcc 19
|||||
Db 8 CCAACCCAGCCTC 20

RESULT 9
US-09-156-163A-10
Sequence 10, Application US/09156163A
Patent No. 6319681
GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
APPLICANT: Fan, Xuedong

APPLICANT: Lundell, Daniel
APPLICANT: Lunn, Charles
APPLICANT: Tan, Jimmy
APPLICANT: Zavadny, Paul
TITLE OF INVENTION: Mammalian TNF-a Convertases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: New Jersey
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 8.1
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/156,163A
FILING DATE: 9/17/98
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/889,909
FILING DATE: July 10, 1997
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: McLaughlin, Jaye P.
REGISTRATION NUMBER: 41,211
REFERENCE/DOCKET NUMBER: J86010B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298 5056
TELEFAX: 908 298 5388
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-156-163A-10

Query Match 65.0%; Score 13; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 7.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 cctaccagctc 19
|||||

Db 8 CCACTCCAGCCTC 20

RESULT 10
US-08-646-538-32
Sequence 32, Application US/08646538
Patent No. 602781
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE: No. 602781 yet assigned
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY:
LOCATION: 1..26
OTHER INFORMATION: /note="oligonucleotide #18990"
US-08-646-538-32

Query Match 64.0%; Score 12.8; DB 3; Length 26;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cactaccagctcc 20
|||

Db 9 CACGTATCAGCCTCC 24

RESULT 11
US-09-503-222-32
Sequence 32, Application US/09503222
Patent No. 6265548
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
TITLE OF INVENTION: Proteins Having Increased Cellular Fluorescence
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,222
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..26
OTHER INFORMATION: /note="oligonucleotide #18990"
US-09-503-222-32

Query Match 64.0%; Score 12.8; DB 4; Length 26;
Best Local Similarity 87.5%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 cactaccagcctcc 20
||| || |||||
Db 9 CACGTATCCAGCCTCC 24

RESULT 12
US-08-646-538-33/C
Sequence 33, Application US/08646538
Patent No. 6027881
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
NUMBER OF SEQUENCES: 37
PROTEINS HAVING INCREASED CELLULAR FLUORESCENCE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE: No. 6027881 yet assigned
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..28
OTHER INFORMATION: /note="oligonucleotide #18991"
US-08-646-538-33

Query Match 64.0%; Score 12.8; DB 3; Length 28;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 cactaccagcctcc 20
||| || |||||
Db 16 CACGTATCCAGCCTCC 1

RESULT 13
US-09-503-222-33/C
Sequence 33, Application US/09503222
Patent No. 6265548
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Galtanaris, George A.
APPLICANT: Stauber, Roland H.
APPLICANT: Vournakis, John N.
TITLE OF INVENTION: Mutant Aequorea victoria Fluorescent
NUMBER OF SEQUENCES: 37
PROTEINS HAVING INCREASED CELLULAR FLUORESCENCE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,222
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,538
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 015280-249000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..28
OTHER INFORMATION: /note="oligonucleotide #18991"
US-09-503-222-33

Query Match 64.0%; Score 12.8; DB 4; Length 28;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 cactaccagcctcc 20
||| || |||||
Db 16 CACGTATCCAGCCTCC 1

RESULT 14

CITY: PALO ALTO
STATE: CALIFORNIA

774-065-13

b 4 GGACCTACCCAGTCTC 19

Search completed: June 28, 2002, 22:16:40
Job time: 8266 sec

Mon Jul 1 08:40:54 2002

us-09-709-170a-3.szlm75.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:10:50 ; Search time 3762.88 Seconds
(without alignments)
183.523 Million cell updates/sec

Title: US-09-709-170A-4

Perfect score: 33
Sequence: 1 acggggaagcgaagcgtggaagtgatcctcgt 33

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_dl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_or:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgc_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	33	100.0	33	6	AR052606	AR052606 Sequence
2	33	100.0	33	6	196085	196085 Sequence 4
3	33	60.6	20	6	AR052605	AR052605 Sequence
4	4	20	60.6	20	196084	196084 Sequence 3
5	5	17.6	53.3	40	AR129866	AR129866 Sequence
6	6	17.6	53.3	40	AR156905	AR156905 Sequence
7	7	16.6	50.3	66	AX337319	AX337319 Sequence
8	8	16.2	49.1	59	AR038054	AR038054 Sequence
9	9	16.2	49.1	59	23	E1115 DNA sequence
10	10	15.6	47.3	51	AX116165	AX116165 Sequence
11	11	15.4	46.7	30	E07533	E07533 Oligonucleo
12	12	15.4	46.7	36	AR044319	AR044319 Sequence
13	13	15.4	46.7	36	6	135959 Sequence 20
14	14	15.4	46.7	36	6	AR082754 Sequence
15	15	15.4	46.7	36	6	AR119736 Sequence
16	16	14.8	44.8	52	6	AR098300 Sequence
17	17	14.6	44.2	31	6	130296 Sequence 6
18	18	14.6	44.2	51	6	AX116661 Sequence
19	19	14.6	44.2	51	6	AX157259 Sequence
20	20	14.6	44.2	72	6	AR030402 Sequence
21	21	14.6	44.2	72	6	AR030402 Sequence
22	22	14.4	43.6	36	6	AR117049 Sequence
23	23	14.4	43.6	48	6	AR117049 Sequence
24	24	14.4	43.6	48	6	AR117050 Sequence
25	25	14.4	43.6	48	6	106472 Sequence 9
26	26	14.4	43.6	48	6	120509 Sequence 37
27	27	14.4	43.6	48	6	120510 Sequence 38
28	28	14.4	43.6	51	6	AX165665 Sequence
29	29	14.4	43.6	51	6	AX189915 Sequence
30	30	14.4	43.6	51	6	188194 Sequence 3
31	31	14.2	43.0	34	9	HMWTCGD2D
32	32	14.2	43.0	51	6	AX204020 Sequence
33	33	14.2	43.0	31	6	AX280500 Sequence
34	34	14.2	43.0	31	6	AX279622 Sequence
35	35	14.2	43.0	49	6	AX279622 Sequence
36	36	14.2	43.0	64	6	AA1972 Sequence 13
37	37	14.2	43.0	67	8	AR163943 Sequence
38	38	14.2	43.0	69	6	AR055068 Sequence
39	39	14.2	43.0	71	8	AR156317 Sequence
40	40	13.8	41.8	26	8	AR163942 Saccharom
41	41	13.8	41.8	27	8	S71818 (5' region,
42	42	13.8	41.8	30	6	AR090965 Sequence
43	43	13.8	41.8	30	6	AR068139 Sequence
44	44	13.8	41.8	30	6	113395 Sequence 5
45	45	13.8	41.8	30	6	113775 Sequence 5
						114876 Sequence 3

ALIGNMENTS

RESULT 1	AR052606	33 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR052606				
DEFINITION	Sequence 4 from patent US 5831066.				
ACCESSION	AR052606				
VERSION	AR052606.1	GI:5975970			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 33)				
AUTHORS	Reed, J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A 03-NOV-1998;				
FEATURES	Location/Qualifiers				
source	1..33				
BASE COUNT	5 a	5 c	10 g	7 t	
ORIGIN					

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0024;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acggggtacggagctggtgtagtcctgt 33
Db 1 ACGGGCTACGGAGCTGGGTAGTGCATCTGT 33

RESULT 2
196085
LOCUS Sequence 4 from patent US 5734033.
DEFINITION
ACCESSION 196085
VERSION 196085.1 GI:3940555
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 33)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 4 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..33
BASE COUNT 5 a 5 c 16 g 7 t

Query Match 100.0%; Score 33; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acggggtacggagctggtgtagtcctgt 33
Db 1 ACGGGCTACGGAGCTGGGTAGTGCATCTGT 33

RESULT 3
AR052605/c
LOCUS Sequence 3 from patent US 5831066.
DEFINITION
ACCESSION AR052605
VERSION AR052605.1 GI:5975969
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 3 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 4 a 10 c 3 g 3 t

Query Match 60.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ggaggtggtgtagtcac 29
Db 20 GGAGGCTGGGTAGTGCATC 1

RESULT 4
196084
LOCUS Sequence 3 from patent US 5734033.
DEFINITION
ACCESSION 196084
VERSION 196084.1 GI:3940554

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 3 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 4 a 10 c 3 g 3 t

Query Match 60.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ggaggtggtgtagtcac 29
Db 20 GGAGGCTGGGTAGTGCATC 1

RESULT 5
AR129866/c
LOCUS Sequence 16 from patent US 6187564.
DEFINITION
ACCESSION AR129866
VERSION AR129866.1 GI:14117763
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Sytkowski,A.J.
TITLE DNA encoding erythropoietin multimers having modified 5' and 3' sequences and its use to prepare EPO therapeutics
JOURNAL Patent: US 6187564-A 16 13-FEB-2001;
FEATURES Location/Qualifiers
source 1..40
BASE COUNT 5 a 19 c 9 g 7 t

Query Match 53.3%; Score 17.6; DB 6; Length 40;
Best Local Similarity 71.9%; Pred. No. 7.4e+03;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 acggggtacggagctggtgtagtcctgt 32
Db 32 ACAGGGGACAGAGCCGGCGGTGTGATCTGG 1

RESULT 6
AR156905/c
LOCUS Sequence 4 from patent US 6242570.
DEFINITION
ACCESSION AR156905
VERSION AR156905.1 GI:15125609
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 40)
AUTHORS Sytkowski,A.J.
TITLE Production and use of recombinant protein multimers with increased biological activity
JOURNAL Patent: US 6242570-A 4 05-JUN-2001;
FEATURES Location/Qualifiers
source 1..40
BASE COUNT 1..40
/Organism="unknown"

8 acgagagctggtagtgatcctg 31
| ||| ||| | |::||| |::|

	57 bp	DNA	PAT 01-SEP-2000
LOCUS	AK082134	linear	
DEFINITION	Sequence 7 from patent US 5976551.		
ACCSSION	M000374		

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:04 ; Search time 1361.16 Seconds
(without alignments)
41.022 Million cell updates/sec

Title: US-09-709-170A-4

Perfect score: 33
Sequence: 1 acggggtaacggagcgtggtgagtcgtcgtgt 33

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	33	16	AA086646
2	33	100.0	33	19	AAV19654
3	20	60.6	20	19	AAV19653
4	18.2	55.2	47	21	AA268500
5	17.6	53.3	35	18	AAV79533
6	17.6	53.3	40	20	AAV25704
7	16.6	50.3	50	21	AAV76605
8	16.2	49.1	45	21	AAV05784
9	16.2	49.1	51	22	AAV34288

10	16.2	49.1	59	17	AAV10693	Trypsin-like enzyme
11	16	48.5	66	22	AAV04737	Synthetic gene shM
12	16	48.5	69	22	AAV03844	Synthetic gene shM
13	15.6	47.3	26	21	AAV57423	Oligonucleotide PC
14	15.6	47.3	51	22	AAV30308	Human SNP oligonuc
15	15.6	47.3	51	22	AAV38492	Human SNP flanking
16	15.4	46.7	30	15	AAV04086	Rad51 primer. Syn
17	15	45.5	51	22	AAV32158	Human SNP oligonuc
18	15	45.5	57	22	AAV0183	Spacer SC-15. Syn
19	14.8	44.8	35	20	AAV21074	Human caveolin pro
20	14.8	44.8	48	17	AAV28625	Quadruplex/duplex
21	14.8	44.8	48	17	AAV28624	Quadruplex/duplex
22	14.6	44.2	23	22	AAV28284	Oligonucleotide SP
23	14.6	44.2	31	19	AAV09157	Preprocrystatin
24	14.6	44.2	33	22	AAV16127	Human VEGF-8167 ma
25	14.6	44.2	45	15	AAV05680	Probe for progenit
26	14.6	44.2	51	22	AAV32214	Human SNP oligonuc
27	14.6	44.2	51	22	AAV173646	Human SNP flanking
28	14.6	44.2	51	22	AAV38988	Human SNP flanking
29	14.6	44.2	62	19	AAV44757	Primer for Human o
30	14.6	44.2	72	16	AAV01280	Exo-cellulohydrol
31	14.4	43.6	24	14	AAV02898	HIA type analysis
32	14.4	43.6	38	20	AAV02137	Human FEN-1 DNA fr
33	14.4	43.6	44	22	AAV61267	A. thaliana dihydr
34	14.4	43.6	48	22	AAV74343	Repetitive protein
35	14.4	43.6	48	22	AAV74344	Oligonucleotide us
36	14.4	43.6	48	22	AAV23379	Oligonucleotide us
37	14.4	43.6	48	22	AAV23380	Oligonucleotide us
38	14.4	43.6	49	16	AAV75496	HPV primer probe H
39	14.4	43.6	50	22	AAV29890	Human SNP oligonuc
40	14.4	43.6	51	22	AAV90214	Human clone c94402
41	14.4	43.6	51	23	AAV00869	Human amino acid c
42	14.4	43.6	56	17	AAV32953	DNA sequence of pr
43	14.4	43.6	59	22	AAV80007	Primer for amplifi
44	14.4	43.6	63	24	AAV98527	Human protective D
45	14.2	43.0	29	21	AAV04062	Polymorphic fragme

ALIGNMENTS

RESULT 1	
AA086646	AA086646 standard; DNA; 33 BP.
ID	AA086646
AC	AA086646
XX	
DT	27-SEP-1995 (first entry)
XX	
DE	Bcl-2 splice donor site.
XX	
KW	Leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
KW	ss.
OS	Synthetic.
XX	
PN	WO9508350-A.
XX	
PD	30-MAR-1995.
XX	
PF	20-SEP-1994; 94WO-US10725.
XX	
PR	20-SEP-1993; 93US-0124256.
XX	
PA	(REED/) REED J C.
XX	
PI	Reed JC;
XX	
DR	WPI; 1995-139394/18.
XX	
PT	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer

XX Disclosure: Page 13; 108bp; English.
 PS
 CC The antisense oligonucleotide SD-AS (AA086645) is complementary to a
 CC portion of the splice donor site of the pre-mRNA coding strand of the
 CC human bcl-2 gene. It reduces the expression of bcl-2 gene product,
 CC thereby inducing programmed cell death of certain cancer cells. The
 CC corresp. bcl-2 sense splice donor site region was synthesized for use
 CC as a control.
 XX
 SQ Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match 100.0%; Score 33; DB 16; Length 33;
 Best Local Similarity 100.0%; Pred. No. 0.00046;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acggggtacggagctggtgtagtgcattcgt 33
 |||||
 Db 1 acggggtacggagctggtgtagtgcattcgt 33

RESULT 2

AAV19654
 ID AAV19654 standard; DNA; 33 BP.

AC AAV19654;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 2.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5734033-A.

PN 31-MAR-1998.

PD 24-MAR-1994; 94US-0288692.

PF 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

XX PS Disclosure; Columns 3-4; 21pp; English.

XX This is a human bcl-2 oligonucleotide based on which an antisense
 CC oligonucleotide complementary to the splice donor site of the human
 CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.

SQ Sequence 33 BP; 5 A; 5 C; 16 G; 7 T; 0 other;

Query Match 100.0%; Score 33; DB 19; Length 33;

Best Local Similarity 100.0%; Pred. No. 0.00046;
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acggggtacggagctggtgtagtgcattcgt 33
 |||||
 Db 1 acggggtacggagctggtgtagtgcattcgt 33

RESULT 3

AAV19653/C
 ID AAV19653 standard; DNA; 20 BP.

AC AAV19653;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 antisense oligonucleotide 2.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

XX Synthetic.

OS Homo sapiens.

XX US5734033-A.

PN 31-MAR-1998.

PD 24-MAR-1994; 94US-0288692.

PF 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

XX (UYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

XX Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

XX PS Claim 6; Columns 3-4; 21pp; English.

XX This antisense oligonucleotide is complementary to the splice donor
 CC site of the human bcl-2 mRNA. The Bcl-2 antisense oligonucleotides are
 CC phosphorothioate derivatives and can straddle strategic sites such as the
 CC translation initiation site, donor and acceptor splicing sites, or sites
 CC for transportation or degradation. Blocking translation at such strategic
 CC sites prevents the formation of a functional bcl-2 gene product. These
 CC oligonucleotides may be used for treating cancers associated with high
 CC levels of bcl-2 gene expression, especially lymphomas and some
 CC leukaemias.

SQ Sequence 20 BP; 4 A; 10 C; 3 G; 3 T; 0 other;

Query Match 60.6%; Score 20; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 62;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 ggaagctggtagtgcattc 29
 |||||
 Db 20 GGAGCTGGTAGTGCATC 1

RESULT 4

AAZ68500/C
 ID AAZ68500 standard; DNA; 47 BP.

AC AAZ68500;

DT	10-SEP-2001	(first entry)
XX		
DE	Human map-related biallelic marker	SEQ ID NO:2847.
XX		
KW	Human genome; biallelic marker; high density disequilibrium map; genomic map; haplotype; phenotype; polymorphic base; genotyping; haploclotyping; hybridisation; identification; characterisation; diagnosis; single nucleotide polymorphism; SNP; ds.	
KM		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	variation	replace(24,C)
FT		/*tag= a
FT		/standard_name= "single nucleotide polymorphism"
XX		
PN	W09954500-A2.	
XX		
PD	28-OCT-1999.	
XX		
PE	21-APR-1999;	99WO-IB00822.
XX		
PR	21-APR-1998;	98US-0082614.
XX	23-NOV-1998;	98US-0109732.
XX		
PA	(GEST) GENSET.	
PI	Cohen D, Blumenfeld M, Chumakov I;	
XX		
DR	WPI: 2000-013267/01.	
XX		
PT	Novel biallelic markers used to construct a high density disequilibrium map of the human genome	-
PS	Claim 3; Page 837; 2745bp; English.	
XX		
CC	AA265654 to AA269578 represent human biallelic markers from the present invention, which contain a polymorphic base at position 24 of their nucleotide sequences. AA269579 to AA277440 represent amplification primers for the biallelic markers. The biallelic markers of the invention have a variety of uses: they can be used for high density mapping of the human genome, and in complex association studies and haploclotyping studies which are useful in determining the genetic basis for disease states. Compositions and methods of the invention can also be useful for the identification of the targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterisation of the differential efficacious responses to and side effects from pharmaceutical agents acting on a disease as well as other treatment.	
CC	N.B. The SEQ. ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and 3367, are not actually given a sequence in the Sequence Listing from the present invention.	
CC		
CC	Sequence 47 BP; 16 A; 13 C; 10 G; 8 T; 0 other;	
XX		
SO		
XX		
Query Match	55.2%;	Score 18.2; DB 21; Length 47;
Best Local Similarity	87.0%;	Pred. No. 3.4e+02;
Matches	20; Conservative 0;	Mismatches 3; Indels 0; Gaps 0;
OY	11 gagctggtagtcgcatcgtgt 33	
DB	42 GGGGCTGTGTAGTTGCATCTGCT 20	
RESULT	5	
ID	AAAT79533	
XX	AAAT79533 standard; DNA; 35 BP.	
XX	AAAT79533;	
DT	06-MAR-1998	(first entry)
XX		

DE	Fos	leucine zipper FR618.
XX		
KM	Protein-protein interaction; interacting polypeptide;	
KM	polypeptide principle; Fos; transcription factor; PCR; primer; ss.	
XX		
OS	Synthetic.	
PN	MO9732017-A1.	
PD	04-SEP-1997.	
XX		
PF	26-FEB-1997; 97WO-EP00931.	
PR	26-FEB-1996; 96EP-0102852.	
XX		
PA	(MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.	
PI	Ge L, Ilaag V;	
XX		
DR	WPI; 1997-448687/41.	
XX		
PT	Identification of interacting polypeptide encoding nucleic acid sequences - e.g. to identify protein-protein interactions, which play an important role in biological processes	
PI		
XX		
PS	Example 6; Page 41; 105pp; English.	
CC		
XX	Primers FR618 (AAT79533) and FR619 (AAT79534) were used in the PCR amplification of DNA encoding the leucine zipper domain of fos	
CC	transcription factor. The PCR product was used to create vector pUC18-IMFfos. This was used in a novel method of identifying	
CC	nucleic acid sequences that encode interacting peptides or proteins. The method involves generating 2 libraries of	
CC	recombinant vectors, expressing members of the libraries in host cells so that at least one interaction is established, and	
CC	selecting for the generation of a screenable or selectable	
CC	property representing the interaction of polypeptides. pUC18-	
CC	IMFfos was used in an experiment to demonstrate selectively	
CC	infective phage (SIP)-based library versus library screening via	
CC	in vitro recombination of separately constructed libraries into	
CC	one phase vector. In this case, the cognate pairing is from the	
CC	interaction between jun and fos.	
XX		
SO	Sequence 35 BP; 1 A; 9 C; 16 G; 9 T; 0 other:	
	Query Match	53.3%; Score 17.6; DB 18; Length 35;
	Best Local Similarity	71.9%; Pred. No. 5.8e+02;
	Matches 23; Conservative	0; Mismatches 9; Indels 0; Gaps
Qy	2 cggggtacgagctcgtgcgtgcacatcgctgt 33 	
Dd	1 cgccgtacgcgcgtctcgtcgtgcgttcgtgt 32	
RESULT 6		
AAX25704/C		
ID	AAX25704 standard; DNA: 40 BP.	
XX		
AC	AAX25704;	
XX		
DT	21-MAY-1999 (first entry)	
XX		
DE	Human erythropoietin homodimer fusion gene primer Epa3-3.	
XX		
KM	Human; erythropoietin; dimer; trimer; polymer; fusion protein; cancer	
KM	biological activity; anemia; proliferation; differentiation; ss;	
KM	progenitor; leucocyte; granulocyte; blood; myelosuppressed patient;	
XX	primer; PCR; amplification.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		

PN WO9902710-A1.
XX
XX 21-JAN-1999.
XX
XX
XX 09-JUL-1998; 98WO-US13944.
XX
XX 03-FEB-1998; 98US-0018138.
PR 10-JUL-1997; 97US-0890929.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PA
XX Sytkowski AJ;
XX
XX WPI; 1999-120911/10.
XX
XX New fusion protein with increased activity comprising at least two
PT protein molecules - used to, e.g. treat erythropoietin related
PT deficiency states for treatment of anaemia
XX
XX Example 1; Page 54; 119pp; English.
XX
XX Primers AA25703-X25708 were used to PCR amplify the human
CC erythropoietin (EPO) gene in order to construct an EPO homodimeric fusion
CC gene (AA25701). The invention relates to the production of dimeric,
CC trimeric or polymeric fusion proteins with increased biological activity.
CC The fusion proteins are used to treat or prevent protein-related
CC deficiency states, specifically, where the protein is erythropoietin
CC (EPO; AA25689), anaemia, but also for increasing proliferation,
CC differentiation and activity of haematopoietic progenitors (e.g. of
CC increasing numbers of leucocytes and granulocytes in the blood of
CC myelosuppressed patients) or for treating cancer and other cell growth
CC disorders.
XX
XX Sequence 40 BP; 5 A; 19 C; 9 G; 7 T; 0 other;
SQ

Query Match 53.3%; Score 17.6; DB 20; Length 40;
Best Local Similarity 71.9%; Pred. No. 5.9e+02;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 acggggtagcggagcgtgtagtgatctctgg 32
Dd 32 ACAAGGACAGACGCCGGCGTGTGATCTGG 1

RESULT 7
ID AAA76605 standard; cDNA; 50 BP.
XX
XX AAA76605;
XX
XX 16-NOV-2000 (first entry)
XX
XX Human clone cg21433543 polymorphic site, SEQ ID NO:288.
DE
XX Human; single nucleotide polymorphism; SNP;
KW detection; identification; gene therapy; ss.
XX
XX Homo sapiens.
OS
XX
XX
PH key Location/Qualifiers
FT variation replace (25..26,AGC)
FT
XX
XX
XX WO200029623-A2.
XX
XX 25-MAY-2000.
XX
XX 17-NOV-1999; 99WO-US27293.
XX
XX 17-NOV-1998; 98US-0109024.
PR 16-NOV-1999; 99US-0109024.
XX

PA (CURA-) CURAGEN CORP.
XX
XX Shinkets RA, Leach MD;
XX
XX WPI; 2000-387826/33.
XX
XX
XX Human nucleic acids containing single nucleotide polymorphisms, useful
PT for treating a subject suffering, or at risk from a pathology due to
PT the presence of a sequence polymorphism -
XX
XX Claim 1; Page 245; 543pp; English.
XX
XX Sequences AA76318-A77509 represent 1192 human nucleic acid sequences
CC which contain single nucleotide polymorphisms (SNPs). Sequences 1 to
CC 1112 (AA76318-A77429) are consecutive pairs of nucleotides which
CC contain silent SNPs. Sequences 1113 to 1192 (AA77430-A77509) are
CC consecutive pairs of nucleotides containing SNPs which result in changes
CC in the corresponding amino acid sequences (AA811749-B11828). The SNPs in
CC sequences 1113 to 1128 (AA77430-A77445) lead to conservative amino acid
CC changes, while those in sequences 1129 to 1186 (AA77446-A77503) result
CC in non-conservative changes. The SNPs in sequences 1187 to 1192
CC (AA77504-A77509) generate frameshift mutations. The invention also
CC relates to a method of detecting a polymorphic site in a nucleic acid and
CC a method of determining the relatedness of two nucleic acids. It also
CC encompasses peptides containing polymorphic sites, antibodies raised
CC against such peptides, and a method of detecting polymorphic
CC proteins/peptides using the antibodies. The nucleic acids are useful for
CC gene therapy of an individual having, suspected of having, or at risk of
CC developing a pathological condition due to the presence of a sequence
CC polymorphism. Such treatment would comprise administration of the
CC wild-type nucleic acid sequence. Antibodies raised against polymorphic
CC peptides can also be used in the treatment of such individuals.
XX
XX Sequence 50 BP; 7 A; 12 C; 20 G; 11 T; 0 other;
SQ

Query Match 50.3%; Score 16.6; DB 21; Length 50;
Best Local Similarity 71.0%; Pred. No. 1.5e+03;
Matches 22; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2 cggggtagcggagcgtggtagtgatctctgg 32
Dd 19 ctgcgtaccgagcgtggtgtagcgtctctgg 49

RESULT 8
ID AAA05784/C
XX AAA05784 standard; DNA; 45 BP.
XX
XX AAA05784;
XX
XX 05-JUN-2000 (first entry)
XX
XX Streptavidin display linker DNA, SEQ ID NO:242.
DE
XX
XX Phage display; bacteriophage M13; fusion protein; major coat protein;
KW protein VIII; phagemid vector; electroporation; combinatorial library;
KW streptavidin; SAV; ss.
XX
XX Synthetic.
OS
XX
XX
XX WO200006717-A2.
XX
XX 10-FEB-2000.
XX
XX 22-JUL-1999; 99WO-US16596.
XX
XX 27-JUL-1998; 98US-0094291.
PR 08-OCT-1998; 98US-0103514.
PR 10-MAY-1999; 99US-0133296.
PR 19-MAY-1999; 99US-0134870.
XX
XX (GENTH) GENENTECH INC.


```
XX (TEIJ ) TEIJUN LTD.
XX Masuda K, Ogawa H, Suga T, Sugimoto Y, Takagi K,
PI Yamacka K, Yasuoka S,
XX WPI: 1996-117356/13.
DR
XX Nucleic acid sequence encoding trypsin-like enzyme - which digests
PT fibrinogen, used as expectorant in treatment of respiratory
PT diseases, e.g. bronchial asthma
XX
PS Example 9; Page 43; 65pp; English.
XX
CC Example 9 describes the cloning of cDNA region encoding
CC trypsin-like enzyme isolated from cough phlegm.
CC Four oligonucleotides are used for PCR: TRY-1 (AAT10694), TRY-8
CC (AAT10695), TRY-10 (AAT10696) and TRY-11 (AAT10697).
CC TRY-1 corresponds to from A1 to A23 of the sequence given in
CC AAT10693, which is part of a cDNA encoding the trypsin-like
CC enzyme. TRY-8 corresponds to from G16 to T40 of AAT10693.
CC TRY-10 is capable of annealing to the 3'-terminus of poly(A)+ RNA.
CC TRY-11 is identical to the 5'-terminus side 19 residues of TRY-10.
CC After amplification, plasmid p19-33 was obtained. p19-33 encodes
CC part of the N-terminus amino acid sequence 20 residues of the
CC trypsin-like enzyme isolated from the cough phlegm (see AAT10698).
XX
SQ Sequence 59 BP; 11 A; 12 C; 26 G; 10 T; 0 other;

Query Match          49.1%; Score 16.2; DB 17; Length 59;
Best Local Similarity 85.7%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ggggtacggagagctggtagg 23
   ||| ||||| ||| |||
Db 8 ggggcacggagagctggtagg 28

RESULT 11
AAS04737/c
ID AAS04737 standard; DNA; 66 BP.
XX
AC AAS04737;
XX
XX 07-SEP-2001 (first entry)
XX
DE Synthetic gene shMOBP/MS, PCR primer #4.
XX
KW shMOBP/MS; PCR primer; ss; immunogenic epitope cluster; IEC;
KW synthetic human myelin-oligodendrocytic basic protein; autoantigen;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; uveitis;
KW autoimmune hepatitis; thyroiditis; orchitis;
KW idiopathic thrombocytopenic purpura; inflammatory disease;
KW Crohn's disease; ulcerative colitis.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO200131037-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-IL00688.
XX
XX 27-OCT-1999; 99IL-0132611.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Ben-Nun A, Kerlero De Rosbo N, Sappler GP;
XX WPI: 2001-300515/31.
XX
DR
```

```
XX Novel synthetic human target autoantigen gene useful for treating
PT autoimmune diseases such as multiple sclerosis, insulin-dependent
PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis
PT
XX
XX Example 5; Fig 26; 182pp; English.
XX
CC The sequence is a PCR primer used in the construction of a nucleic acid
CC encoding shMOBP/MS (synthetic human myelin-oligodendrocytic
CC basic protein containing immunogenic epitope clusters (IEC) from MOBP.
CC The synthetic human target autoantigen genes of the invention comprise
CC sequences coding for at least 2 IECs of autoantigen(s) related to a
CC specific autoimmune disease. The synthetic human target autoantigen genes
CC are useful for treating autoimmune diseases such as multiple sclerosis,
CC insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia
CC gravis, uveitis, autoimmune hepatitis, thyroiditis, orchitis,
CC idiopathic thrombocytopenic purpura, and inflammatory diseases (Crohn's
CC disease, ulcerative colitis). The synthetic human target autoantigen
CC genes are also useful for diagnosis and/or monitoring the progression of
CC the autoimmune disease.
XX
SQ Sequence 66 BP; 17 A; 28 C; 15 G; 6 T; 0 other;
```

```
Query Match          48.5%; Score 16; DB 22; Length 66;
Best Local Similarity 68.8%; Pred. No. 2.6e+03;
Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY 1 acgggtacggagagctggtagtgcatctgg 32
   ||| ||||| ||||| ||| |||
Db 40 ACTTGCAACGGCGGCTGTGACCGCTCTTCTGG 9
```

```
RESULT 12
AAS03844/c
ID AAS03844 standard; DNA; 69 BP.
XX
AC AAS03844;
XX
XX 07-SEP-2001 (first entry)
XX
DE Synthetic gene shMOBP/E, PCR primer #4.
XX
KW shMOBP/E; PCR primer; ss; immunogenic epitope cluster; IEC;
KW synthetic human myelin-oligodendrocytic basic protein; autoantigen;
KW autoimmune disease; multiple sclerosis; rheumatoid arthritis;
KW insulin-dependent diabetes mellitus; myasthenia gravis; uveitis;
KW autoimmune hepatitis; thyroiditis; orchitis;
KW idiopathic thrombocytopenic purpura; inflammatory disease;
KW Crohn's disease; ulcerative colitis.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO200131037-A2.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-IL00688.
XX
XX 27-OCT-1999; 99IL-0132611.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Ben-Nun A, Kerlero De Rosbo N, Sappler GP;
XX WPI: 2001-300515/31.
XX
XX Novel synthetic human target autoantigen gene useful for treating
PT autoimmune diseases such as multiple sclerosis, insulin-dependent
PT diabetes mellitus, rheumatoid arthritis, myasthenia gravis, and uveitis
PT
```

PS Example 2; Fig 9; 182bp; English.

XX The sequence represents a PCR primer used in the construction of
CC a nucleic acid encoding shOBP/E (synthetic human myelin-oligodendrocytic
CC basic protein containing immunogenic epitope clusters (IEC) from MOBP.
CC The synthetic human target autoantigen genes of the invention comprise
CC sequences coding for at least 2 IECs of autoantigen(s) related to a
CC specific autoimmune disease. The synthetic human target autoantigen genes
CC are useful for treating autoimmune diseases such as multiple sclerosis,
CC insulin-dependent diabetes mellitus, rheumatoid arthritis, myasthenia
CC gravis, uveitis, autoimmune hepatitis, thyroiditis, insulinitis, orchitis,
CC idiopathic thrombocytopenic purpura, and inflammatory diseases (Crohn's
CC disease, ulcerative colitis). The synthetic human target autoantigen
CC genes are also useful for diagnosis and/or monitoring the progression of
CC the autoimmune disease.

XX Sequence 69 BP; 21 A; 21 C; 19 G; 8 T; 0 other;

Query Match 48.5%; Score 16; DB 22; Length 69;

Best Local Similarity 68.8%; Pred. No. 2.6e+03;

Matches 22; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

0Y 1 acggggtagcgagcggtggtgagtcgacatcg 32

DB 64 ACTTGGCAGCGCGGTGCTGCTCTTCG 33

RESULT 13

AAZ57423/C

ID AAZ57423 standard; DNA; 26 BP.

AC AAZ57423;

XX 07-APR-2000 (first entry)

DE Oligonucleotide PCR primer pair #3 primer #1.

XX PCR primer; Zaocys dhumade; Tortoise plastron; Oviductus ranae;

KW discrimination; black snake; forest frog; oil; reagent box;

KW medicinal; ss.

XX Synthetic.

XX CN1232085-A.

XX 20-OCN-1999.

XX 31-MAR-1999; 99CN-0114133.

XX 31-MAR-1999; 99CN-0114133.

XX (UYNA-) UNIV NANJING.

XX Wang Y, Zhou K, Liu Z;

XX WPI; 2000-098492/09.

XX Polymerase chain reaction (PCR) determining primer for Zaocys dhumade,

XX Tortoise plastron and Oviductus ranae -

XX Claim 1; Page 1; 4pp; Chinese.

XX The present invention describes a special DNA sequence which can be used
CC to synthesise three pairs of high-specificity primers useful for
CC discriminating if black snake, tortoise plastron and forest frog oil are
CC true or false by simple polymerase chain reaction (PCR) of their DNA.
CC AAZ57419 to AAZ57424 represent specifically claimed primers from the
CC present invention. The primers can be used to make a reagent box for
CC discriminating medicinal materials with high speed and quality.

XX Sequence 26 BP; 6 A; 12 C; 1 G; 7 T; 0 other;

Query Match 47.3%; Score 15.6; DB 21; Length 26;

Best Local Similarity 81.8%; Pred. No. 3.5e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

0Y 11 gagcgtgtagtcgacatcg 32

DB 22 GAGCATGCTTGATGATCGG 1

RESULT 14

AAI30308

ID AAI30308 standard; DNA; 51 BP.

AC AAI30308;

XX 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #3516.

XX Immunosuppressive; immunostimulatory; antinflammatory; cytostatic;

KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;

KW amyloid protein; angiotensin; apoptosis related protein; cadherin;

KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KW complement related protein; cytochrome; kinesis; cytokine; interferon;

KW interleukin; G-protein coupled receptor; thioesterase; inflammation;

KW multifactorial disease; autoimmune disease; infection;

KW nervous system disease; ss.

XX Homo sapiens.

XX WO200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shinkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,

XX oncogenes and histones, useful for diagnosing and treating, e.g.

XX cancer, autoimmune diseases and infections -

XX Claim 1; Page 2394; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC histones, kinases, colony stimulating factors, complement related
CC proteins, cytochromes, kinesis, cytokines, interferons, interleukins,
CC G-protein coupled receptors and thioesterases. The present sequence is
CC one such oligonucleotide. The oligonucleotides and the peptides encoded
CC by them may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate expression of the proteins listed
CC above. Disorders that may be prevented, diagnosed and/or treated include
CC multifactorial diseases with a genetic component, such as autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC (e.g. cancers of the bladder, brain, breast, colon and kidney, cancer
CC leukemia), diseases of the nervous system and an infection of pathogenic
CC organisms.

XX Sequence 51 BP; 13 A; 10 C; 19 G; 9 T; 0 other;

Mon Jul 1 08:40:55 2002

us-09-709-170a-4.szlm75.rng

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:40 ; Search time 334.55 Seconds
(without alignments)
24.229 Million cell updates/sec

Title: US-09-709-170A-4

Perfect score: 33

Sequence: 1 aacgggtacagagctggtgtagtgcattgt 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	33	100.0	33 1 US-08-217-082A-4	Sequence 4, Appl
2	33	100.0	33 2 US-08-465-485A-4	Sequence 4, Appl
3	33	100.0	33 3 US-09-080-285-4	Sequence 4, Appl
4	20	60.6	20 1 US-08-217-082A-3	Sequence 3, Appl
5	20	60.6	20 2 US-08-465-485A-3	Sequence 3, Appl
6	20	60.6	20 3 US-09-080-285-3	Sequence 3, Appl
7	17.6	53.3	40 4 US-09-018-138-16	Sequence 16, Appl
8	17.6	53.3	40 4 US-08-890-929-4	Sequence 4, Appl
9	16.2	49.1	59 1 US-08-508-448C-4	Sequence 4, Appl
10	15.4	46.7	36 1 US-08-411-795B-200	Sequence 200, App
11	15.4	46.7	36 1 US-08-466-319A-200	Sequence 200, App
12	15	45.5	37 2 US-08-484-905-7	Sequence 7, Appl
13	15	45.5	37 2 US-08-481-985B-7	Sequence 7, Appl
14	15	45.5	57 3 US-08-370-476-7	Sequence 7, Appl
15	14.8	44.8	35 4 US-09-264-693-6	Sequence 6, Appl
16	14.8	44.8	48 5 PCT-US95-11985A-30	Sequence 30, Appl
17	14.8	44.8	48 5 PCT-US95-11985A-31	Sequence 31, Appl
18	14.8	44.8	31 3 US-08-648-322-13	Sequence 13, Appl
19	14.6	44.2	45 1 US-08-294-770A-6	Sequence 6, Appl
20	14.6	44.2	45 2 US-08-448-735C-6	Sequence 6, Appl
21	14.6	44.2	62 4 US-08-994-962-9	Sequence 9, Appl
22	14.6	44.2	72 2 US-08-169-948B-17	Sequence 17, Appl
23	14.6	44.2	72 2 US-08-448-873-17	Sequence 17, Appl
24	14.6	44.2	72 2 US-08-382-452D-17	Sequence 17, Appl
25	14.4	43.6	36 2 US-08-750-128-10	Sequence 10, Appl
26	14.4	43.6	38 2 US-08-455-968E-48	Sequence 48, Appl
27	14.4	43.6	48 1 US-07-609-716-37	Sequence 37, Appl

C	28	14.4	43.6	48 1	US-07-609-716-38	Sequence 38, Appl
C	29	14.4	43.6	48 3	US-08-475-411A-37	Sequence 37, Appl
C	30	14.4	43.6	48 3	US-08-475-411A-38	Sequence 38, Appl
C	31	14.4	43.6	48 4	US-08-478-029A-37	Sequence 37, Appl
C	32	14.4	43.6	48 4	US-08-478-029A-38	Sequence 38, Appl
C	33	14.4	43.6	49 5	PCT-US94-05085A-27	Sequence 27, Appl
C	34	14.4	43.6	49 5	PCT-US94-05085A-27	Sequence 27, Appl
C	35	14.4	43.6	56 1	US-08-344-820-3	Sequence 3, Appl
C	36	14.4	43.6	66 3	US-08-478-097A-34	Sequence 34, Appl
	37	14	42.4	24 5	PCT-US95-11985A-22	Sequence 22, Appl
	38	14	42.4	24 5	PCT-US95-11985A-25	Sequence 25, Appl
	39	14	42.4	24 5	PCT-US95-11985A-35	Sequence 35, Appl
	40	14	42.4	36 4	US-09-041-878-2	Sequence 2, Appl
	41	14	42.4	39 3	US-09-042-105-27	Sequence 18, Appl
	42	14	42.4	60 5	PCT-US95-11985A-18	Sequence 81, Appl
	43	14	42.4	69 2	US-08-790-963-81	Sequence 81, Appl
	44	14	42.4	69 4	US-09-371-77A-81	Sequence 32, Appl
C	45	13.8	41.8	26 3	US-08-646-538-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-217-082A-4
; Sequence 4, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/286,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
US-08-217-082A-4

Query Match 100.0%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgcattgt 33
|||||
Db 1 ACGGGTTACGGAGCTGGTAGTGCATCTGCT 33

RESULT 2

US-08-465-485A-4
; Sequence 4, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-465-485A-4

Query Match 100.0%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgcattgt 33
|||||
Db 1 ACGGGTTACGGAGCTGGTAGTGCATCTGCT 33

RESULT 3
US-09-080-285-4
; Sequence 4, Application US/09080285

; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-4

Query Match 100.0%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgcattgt 33
|||||
Db 1 ACGGGTTACGGAGCTGGTAGTGCATCTGCT 33

RESULT 4
US-08-217-082A-3/C
; Sequence 3, Application US/08217082A

; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.

STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/217,082A
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-3

Query Match 60.6%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ggaagctggtgtagtcac 29
|||||
DB 20 GGAGCTGGTGGTGCATC 1

RESULT 5
US-08-465-485A-3/C
Sequence 3, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-3

Query Match 60.6%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ggaagctggtgtagtcac 29
|||||
DB 20 GGAGCTGGTGGTGCATC 1

RESULT 6
US-09-080-285-3/C
Sequence 3, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2070
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-3

Query Match
Best Local Similarity 60.6%; Score 20; DB 3; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 ggaagctggtagtgatc 29
|||||
DB 20 GGAGCGGTGAGTGCAATC 1

RESULT 7
US-09-018-138-16/c
Sequence 16, Application US/09018138
Patent No. 6187564
GENERAL INFORMATION:
APPLICANT: Sytkowski, Arthur J.
TITLE OF INVENTION: Production and Use of Recombinant
FILE REFERENCE: B1H97-05A
CURRENT APPLICATION NUMBER: US/09/018,138
EARLIER FILING DATE: 1998-02-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 40
TYPE: DNA
ORGANISM: Human
US-09-018-138-16

Query Match
Best Local Similarity 53.3%; Score 17.6; DB 4; Length 40;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgatc 32
|||||
DB 32 ACAGGGGACAGAGCCGGGGTGTGATCTGC 1

RESULT 8
US-08-890-929-4/c
Sequence 4, Application US/08890929A
Patent No. 6242570
GENERAL INFORMATION:
APPLICANT: Sytkowski, Arthur J.
TITLE OF INVENTION: PRODUCTION AND USE OF RECOMBINANT
FILE REFERENCE: B1H97-05
CURRENT APPLICATION NUMBER: US/08/890,929A
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 40

TYPE: DNA
ORGANISM: Synthetic
US-08-890-929-4

Query Match
Best Local Similarity 53.3%; Score 17.6; DB 4; Length 40;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 acggggtacggagctggtagtgatc 32
|||||
DB 32 ACAGGGGACAGAGCCGGGGTGTGATCTGC 1

RESULT 9
US-08-508-448C-4
Sequence 4, Application US/08508448C
Patent No. 5804410
GENERAL INFORMATION:
APPLICANT: Kazuyoshi YAMAKA et al.
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE ENCODING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,448C
FILING DATE: July 28, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: trachea
US-08-508-448C-4

Query Match
Best Local Similarity 49.1%; Score 16.2; DB 1; Length 59;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ggggtacggagctggtagt 23
|||||
DB 8 GGGGACGAGGCTGAGAGG 28

RESULT 10

```

APPLICANT: Bratford-Goldberg, Sarah R.
APPLICANT: Caparon, Mairé H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kumnan
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Interleukin-3 (IL-3) Multiple Mutation
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 415
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,319A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,044
FILING DATE: 24-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11197
FILING DATE: 22-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C2713/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 200:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-469-319A-200

Query Match          46.7%; Score 15.4; DB 1; Length 36,
Best Local Similarity 66.7%; Pred. No. 9,2e+02;
Matches 22; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

cy      1  acggagtcagcggagcctggtagtgcatactggt 33
        | | | | | | | | | | | | | | | | | |
Db      2  AGGTTGTCGGGTCCAGGCAAGGTCCAGAGTGCT 34

RESULT 12
US-08-484-905-7
; Sequence 7, Application US/08484905
; Patent No. 5976551
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Koulitsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/92,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-905-7

Query Match 45.5%; Score 15; DB 2; Length 57;
Best Local Similarity 67.7%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 ggggtacgagagctcgggtaggtgcatcgtgt 33
||| ||| | | | | | | | | | | | | | | | |
Db 9 gggatcgatccgacgacgctggtcgatccgct 39

RESULT 13
US-08-481-985B-7
Sequence 7, Application US/08481985B
Patent No. 6011146
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/92,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-481-985B-7

Query Match 45.5%; Score 15; DB 3; Length 57;
Best Local Similarity 67.7%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 ggggtacgagagctcgggtaggtgcatcgtgt 33
||| ||| | | | | | | | | | | | | | | | |
Db 9 gggatcgatccgacgacgctggtcgatccgct 39

RESULT 14
US-08-370-476-7
Sequence 7, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818
 FILING DATE: 05-DEC-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/792,473
 FILING DATE: 15-NOV-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 05243.0001-01000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-370-476-7

Query Match 45.5%; Score 15; DB 3; Length 57;
 Best Local Similarity 67.7%; Pred. No. 1.3e+03;
 Matches 21; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

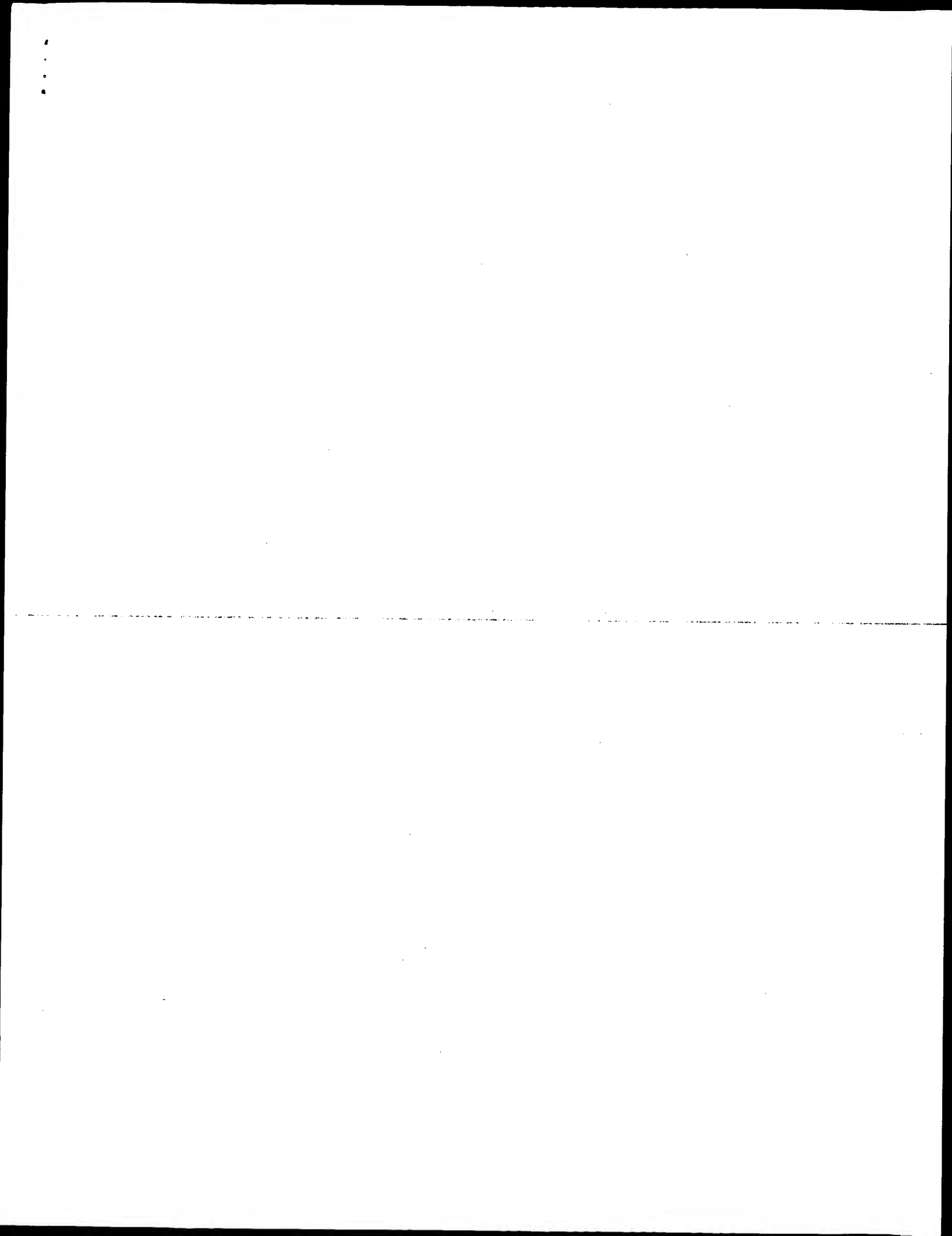
Oy 3 ggagtcaggagctggtagtcacatctgt 33
 |||| |||| | | |||| |||| ||||
 Db 9 GGGGATCGGATCCGAGCGCGTGATCCGCT 39

RESULT 15
 US-09-264-693-6/c
 ; Sequence 6, Application US/09264693
 ; Patent No. 6261760
 ; GENERAL INFORMATION:
 ; APPLICANT: Fielding, Christopher E
 ; APPLICANT: Fielding, Phoebe E
 ; TITLE OF INVENTION: REGULATION OF THE CELL CYCLE BY STEROLS
 ; FILE REFERENCE: 2500.141US1 Regulation of cell cycle
 ; CURRENT APPLICATION NUMBER: US/09/264,693
 ; EARLIER FILING DATE: 1999-03-08
 ; EARLIER APPLICATION NUMBER: 60/077,351
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 35
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Probe cav-646
 US-09-264-693-6

Query Match 44.8%; Score 14.8; DB 4; Length 35;
 Best Local Similarity 73.1%; Pred. No. 1.6e+03;
 Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 8 acggagagctggtagtcacatctgt 33
 |||| |||| | | |||| |||| ||||
 Db 35 AAGGATCTGTGTGGTGGCTGTGCT 10

Search completed: June 28, 2002, 22:16:41
 Job time: 8267 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using sw model

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Run on:      June 28, 2002, 22:10:53 ; Search time 3762.88 Seconds
              (without alignments)
              111.226 Million cell updates/sec
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Title: US-09-709-170A-5
Perfect score: 20
Sequence: 1 acaagcattcctgcagltg 20

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 7944322
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Minimum DB seq length: 0
Maximum DB seq length: 75
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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2: gb.hg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
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29: em.vi.*
30: em.hg_hum.*
31: em.hg_inv.*
32: em.hg_other.*
33: em.hgo_inv.*
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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID

					Description

C	4	3	20	100.0	20	6	AR052607	Sequence 5
C	4	3	20	100.0	20	6	AR052608	Sequence 6
C	5	15.2	76.0	100.0	36	6	AR109687	Sequence 6
C	6	13.8	67.0	27	6	AR109683	Sequence	
C	7	13.4	67.0	21	6	AR109666	Sequence	
C	8	13.4	67.0	27	6	AX306472	Sequence	
C	9	13.4	67.0	30	6	AR109665	Sequence	
C	10	13.2	66.0	27	6	AR109713	Sequence	
C	11	13.2	66.0	30	6	AX15337	oligonucleo	
C	12	13.2	66.0	70	9	AX041996	Sequence	
C	13	12.8	64.0	21	6	S60091	Sequence	
C	14	12.8	64.0	21	6	E36783	Novel phoH	
C	15	12.8	64.0	21	23	E12037	PCR primer	
C	16	12.8	64.0	27	6	AR109662	Sequence	
C	17	12.8	64.0	30	6	AR109714	Sequence	
C	18	12.6	63.0	39	6	AX183967	Sequence	
C	19	12.6	63.0	24	6	AX292703	Sequence	
C	20	12.6	63.0	28	6	AR023947	Sequence	
C	21	12.6	63.0	28	6	I12125	Sequence 30	
C	22	12.6	63.0	28	6	I15448	Sequence 26	
C	23	12.6	63.0	28	6	I41295	Sequence 30	
C	24	12.6	63.0	29	6	AR160598	Sequence	
C	25	12.6	63.0	30	6	AR130336	Sequence	
C	26	12.6	63.0	31	6	AR137727	Sequence	
C	27	12.6	63.0	33	6	AR066581	Sequence	
C	28	12.6	63.0	33	6	I70304	Sequence 7	
C	29	12.6	63.0	39	6	A51349	Sequence 34	
C	30	12.6	63.0	46	6	AR164998	Sequence	
C	31	12.6	63.0	47	12	SYNNAVC		
C	32	12.6	63.0	57	6	E49832	Avian neovi	
C	33	12.6	63.0	57	9	HSTCRA021	Substrate f	
C	34	12.6	63.0	60	6	I87862	Human mRNA	
C	35	12.6	63.0	60	9	HSADCD2517	Sequence 15	
C	36	12.6	63.0	66	9	HUMCTRAL7	LF0000097 Homo sapi	
C	37	12.6	63.0	70	6	AX036029	Human reart	
C	38	12.6	63.0	71	6	AX008541	Sequence	
C	39	12.4	62.0	19	6	AX201462	Sequence	
C	40	12.4	62.0	21	6	A09412	Nucleotide	
C	41	12.4	62.0	21	6	A09477	DNA fragmen	
C	42	12.4	62.0	21	6	A09482	DNA fragmen	
C	43	12.4	62.0	22	6	AX298468	Sequence	
C	44	12.4	62.0	29	6	A50697	Sequence 36	
C	45	12.4	62.0	29	6	AR083328	Sequence	
				31	6	AX249197	Sequence	

[illegible]

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgacgtg 20
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Db 1 ACAAGCCTCCTGCAGTTG 20

RESULT 2
LOCUS 196086
DEFINITION Sequence 5 from patent US 5734033.
ACCESSION 196086
VERSION 196086.1 GI:3940556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 5 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 6 a 5 c 5 g 4 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.7; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgacgtg 20
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Db 1 ACAAGCCTCCTGCAGTTG 20

RESULT 3
LOCUS AR052608
DEFINITION Sequence 6 from patent US 5831066.
ACCESSION AR052608
VERSION AR052608.1 GI:5975972
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 6 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..36
/organism="unknown"

BASE COUNT 7 a 11 c 10 g 8 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgacgtg 20
|||||
Db 24 ACAAGCCTCCTGCAGTTG 5

RESULT 4
LOCUS 196087
DEFINITION Sequence 6 from patent US 5734033.
ACCESSION 196087
VERSION 196087.1 GI:3940557

BASE COUNT 36 bp DNA 1 linear PAT 01-DEC-1998

ORIGIN

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 6 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..36
/organism="unknown"

BASE COUNT 7 a 11 c 10 g 8 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 5.6; 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgacgtg 20
|||||
Db 24 ACAAGCCTCCTGCAGTTG 5

RESULT 5
LOCUS AR109663
DEFINITION Sequence 87 from patent US 6114139.
ACCESSION AR109663
VERSION AR109663.1 GI:12825939
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 87 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"

BASE COUNT 3 a 7 c 5 g 12 t

ORIGIN

Query Match 76.0%; Score 15.2; DB 6; Length 27;
Best Local Similarity 85.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 acaagcctcctgacgtg 20
|||||
Db 25 ACAAGCCTCCTGCAGATG 6

RESULT 6
LOCUS AR109666
DEFINITION Sequence 90 from patent US 6114139.
ACCESSION AR109666
VERSION AR109666.1 GI:12825942
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 90 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"

BASE COUNT 2 a 7 c 6 g 12 t

ORIGIN

REFERENCE 1 (bases 1 to 30)
AUTHORS Nelson, P. S., Hood, L., and Lin, B.
TITLE Prostate-specific polynucleotides, polypeptides and their methods of use
JOURNAL Patent: WO 0065067-A, 26 02-NOV-2000;
The University of Washington (US)
FEATURES
source
1. .30
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/note="PRC Primer"
misc_binding
1. .30
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BASE COUNT 8 a 7 c 5 g 10 t
ORIGIN

Query Match 66.0%; Score 13.2; DB 6; Length 30;
Best Local Similarity 83.3%; Pred. No. 3.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 caaagcactcgcagtt 19
||||| ||||| ||| |||
Db 7 CAAGCCATCTTGCTGT 24

RESULT 12
S60091 70 bp mRNA linear PRI 23-JUL-1993
LOCUS dystrophin (exon 43 directly spliced to exon 45) [human,
DEFINITION lymphocytes, mRNA Partial Mutant, 70 nt].
ACCESSION S60091
VERSION S60091
KEYWORDS S60091.1 GI:300170
SOURCE human lymphocytes.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 70)
Narita, N., Nishio, H., Kitoh, Y., Ishikawa, Y., Ishikawa, Y.,
Minami, R., Nakamura, H. and Matsuo, M.
Insertion of a 5' truncated element into the 3' end of exon 44
of the dystrophin gene resulted in skipping of the exon during
splicing in a case of Duchenne muscular dystrophy
J. Clin. Invest. 91 (5), 1862-1867 (1993)
JOURNAL 93253023
MEDLINE
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gblbgs 131496] from the original journal article.
FEATURES
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1. .70
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1. .70
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/codon_start=1
/protein_id="AADI13910.1"
/db_xref="GI:4261610"
/translation="DROGNSRNALGSGKLSBH"
BASE COUNT 22 a 15 c 21 g 12 t
ORIGIN

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Best Local Similarity 83.3%; Pred. No. 3.4e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 caaagcactcgcagtt 19
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Db 32 CAATGCATCTTGAGATT 15

RESULT 13
E36783
LOCUS Novel phoH. 21 bp DNA linear PAT 07-FEB-2001
DEFINITION Novel phoH.
E36783
ACCESSION E36783
VERSION E36783.1 GI:13022751
KEYWORDS JP 1999253175-A/3.
SOURCE JP 1999253175-A/3.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Magudarena, S.J.R.R.
TITLE Novel phoH
JOURNAL Patent: JP 1999253175-A 3 21-SEP-1999;
SMITHKLINE BEECHAM CORP
COMMENT OS Unidentified
PN JP 1999253175-A/3
PD 21-SEP-1999
PF 18-SEP-1998 JP 1998303154
PI 18-SEP-1997 US 08/932978
PI MAGUDARENA SARA KAIN, JAMES RAYMOND BURAU
PC C12N15/09, A61K31/00, A61K38/00, A61K39/395, C12P21/02, C12Q1/68,
PC GO1N33/15,
PC C12R1:46) PC, C12N15/00,
PC A61K37/02, (C12N15/00, C12R1:46)
CC Strandedness: Single;
CC Topology: Linear;
FH Key
FT source
1. .21
Location/Qualifiers
1. .21
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source
1. .21
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/db_xref="taxon:32644"
BASE COUNT 8 a 6 c 4 g 3 t
ORIGIN

Query Match 64.0%; Score 12.8; DB 6; Length 21;
Best Local Similarity 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acaagcactcgcag 16
||||| ||||| ||| |||
Db 1 ACAAGCCTATCA 16

RESULT 14
E12037/c standard; DNA; UNC; 21 BP.
ID E12037
XX E12037;
AC E12037;
XX E12037;
SV E12037.1
XX
XX
DT 08-OCT-1997 (Rel. 52, Created)
DT 02-SEP-2000 (Rel. 65, Last updated, Version 2)
DE PCR primer for detecting human tyrosine phosphatase, PTP-U2.
XX
XX
KW JP 1996242852-A/5.
XX
XX
OS unidentified
OC unclassified.
XX
XX
RN 1-21
RP
RA Tsuruo T., Kiyomitsu H.;
RT "TYROSINE DEPHOSPHORYLATION ENZYME AND GENE CODING FOR THE ENZYME";
RL Patent number JP1996242852-A/5, 24-SEP-1996.

RL MITSUBISHI CHEM CORP.

XX OS None
CC OC Artificial sequences.
CC PN JP 1996242852-A/5
CC PD 24-SEP-1996
CC PF 10-MAR-1995 JP 1995051374
CC PI TSURUO TAKASHI, KIYOMIYA HIROXUKI
CC PC C12N9/12,C12N1/21,C12N15/09,(C12N9/12,C12R1:19),(C12N9/12,
CC PC C12R1:91),
CC PC (C12N1/21,C12R1:19);
CC CC strandedness: Single;
CC CC topology: linear;
CC CC hypothetical: No;
CC CC anti-sense: Yes;
CC CC Key Location/Qualifiers
CC FH 1..21
CC FT source /organism="Artificial sequences"
XX FT
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FH source 1..21
FT /db_xref="taxon:32644"
FT /organism="unidentified"
XX SQ Sequence 21 BP; 6 A; 5 C; 4 G; 6 T; 0 other;

Query Match

Best Local Similarity 64.0%; Score 12.8; DB 23; Length 21;
Matches 14; Conservative 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 aagcatcctgcagt 19
||| |||||
Db 17 AAGTATCCTGCAGTT 2

RESULT 15

ARI09662/C ARI09662 27 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 86 from patent US 6114139.
ACCESSION ARI09662
VERSION ARI09662.1 GI:12825938
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)

AUTHORS Hinuma,S., Hosoya,M., Fujii,R., Ohtaki,T., Fukusumi,S. and Ohgi,K.
TITLE G-protein coupled receptor protein and a DNA encoding the receptor
JOURNAL Patent: US 6114139-A 86 05-SEP-2000;
FEATURES Location/Qualifiers
source 1..27
/organism="unknown"

BASE COUNT 0 a 8 c 7 g 12 t
ORIGIN

Query Match

Best Local Similarity 64.0%; Score 12.8; DB 6; Length 27;
Matches 14; Conservative 87.5%; Pred. No. 5.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acaagcatcctgca 16
|||||
Db 25 ACAAGCAGCAGCA 10

Search completed: June 28, 2002, 22:10:56
Job time: 8347 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:06 ; Search time 1381.16 Seconds
(without alignments)
24.862 Million cell updates/sec

Title: US-09-709-170a-5

Perfect score: 20

Sequence: 1 acaagagcatcctgcagttg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*

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- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20 19 AAV19655	Human bcl-2 antise
2	20	100.0	36 16 AAG86648	bcl-2 splice accep
3	20	100.0	36 19 AAV19656	Human bcl-2 oligon
4	14.8	74.0	40 21 AAC63894	Chinese hamster/ra
5	14.8	74.0	51 22 AAL32869	Human SNP oligonuc
6	14.2	71.0	30 21 AAAG9234	Upstream primer fo
7	14.2	71.0	41 21 AAZ36900	PCR primer used to
8	13.6	68.0	45 19 AAV36324	Human GABA recepto
9	13.6	68.0	57 14 AAO34907	PCR primer #63 use

10	13.6	68.0	57 18 AAV77691	Staphylococcus aur
11	13.4	67.0	20 20 AAV69904	PCR primer used to
12	13.4	67.0	21 20 AAD26507	898001 PCR primer
13	13.2	66.0	20 21 AAD00976	Primer #2 for TOPP
14	13.2	66.0	30 21 AAC83346	Primer U75329-71R.
15	13	65.0	30 21 AAT02537	Vaccinia virus ORF
16	13	65.0	43 16 AAT02537	Human SNP oligonuc
17	12.8	64.0	50 22 AAL29366	Human tyrosine dep
18	12.8	64.0	21 17 AAT48483	Streptococcus pneu
19	12.8	64.0	21 20 AAL19906	Oligonucleotide M1
20	12.8	64.0	23 20 AAZ25698	Human ppr-1 gene e
21	12.8	64.0	25 22 AAT6064	PIg BDNF cDNA prob
22	12.8	64.0	30 16 AAO93139	Human single nucle
23	12.8	64.0	31 22 AAI31007	Human inflammatory
24	12.8	64.0	39 22 AAH91394	Staphylococcus aur
25	12.6	63.0	74 18 AAV77660	Homo sapiens BARD1
26	12.6	63.0	21 19 AAV24200	Homo sapiens induc
27	12.6	63.0	24 22 AAF44587	Mouse DBS-induced
28	12.6	63.0	24 24 AB191326	Capture oligonucle
29	12.6	63.0	24 24 AB191327	Sequence of forward
30	12.6	63.0	28 13 AAO22070	Oligonucleotide pri
31	12.6	63.0	28 13 AAO24348	Probe used to scre
32	12.6	63.0	29 20 AAX81807	Human IAPP gene pr
33	12.6	63.0	30 18 AAT43800	Bacteriophage lamb
34	12.6	63.0	31 22 AAD07160	Bacteriophage lamb
35	12.6	63.0	31 22 AAF74954	MCP-n5 PCR primer.
36	12.6	63.0	33 16 AAO87501	pc4FC-METH1 PCR pr
37	12.6	63.0	43 22 AAC90375	Probe used to isol
38	12.6	63.0	45 11 AAO06062	OmpC His-tag fusio
39	12.6	63.0	46 22 AAT75621	HIV protease detec
40	12.6	63.0	57 22 AAF81686	Primer AS6 for mou
41	12.6	63.0	60 19 AAV13217	B. subtilis lunazi
42	12.6	63.0	70 21 AAA98079	Synthetic RNA olig
43	12.4	62.0	71 21 AAZ55875	Murine SMC1 gene-s
44	12.4	62.0	22 24 AAS97492	Human dystrophin g
45	12.4	62.0	31 22 AAC83660	HTLV-1 capture pro

ALIGNMENTS

RESULT	ID	AAV19655 standard; DNA: 20 BP.
1	AAV19655	
AC	AAV19655:	
XX		
DT	12-JUN-1998	(first entry)
XX		
DE	Human bcl-2 antisense oligonucleotide 3.	
XX		
KW	Antisense oligonucleotide: bcl-2 gene; lymphoma; leukaemia; human;	
KW	cancer; ss.	
XX		
OS	Synthetic.	
OS	Homo sapiens.	
XX		
PN	US5734033-A.	
XX		
PD	31-MAR-1998.	
XX		
PF	24-MAR-1994;	94US-0288692.
XX		
PR	21-FEB-1992;	92US-0840716.
PR	22-DEC-1988;	88US-0288692.
XX	24-MAR-1994;	94US-0217082.
PA	(UYPE-) UNIV PENNSYLVANIA.	
XX		
PI	Reed J;	
XX		
DR	WPI; 1998-229881/20.	

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Claim 6; Columns 3-4; 21pp; English.

CC This antisense oligonucleotide is complementary to the splice acceptor
site of the human bcl-2 mRNA. The bcl-2 antisense oligonucleotides are
phosphorothioate derivatives and can straddle strategic sites such as the
translation initiation site, donor and acceptor splicing sites, or sites
for transportation or degradation. Blocking translation at such strategic
sites prevents the formation of a functional bcl-2 gene product. These
oligonucleotides may be used for treating cancers associated with high
levels of bcl-2 gene expression, especially lymphomas and some
leukaemias.

CC Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaagcctcctgcagttg 20
|||||
Db 1 acaagcctcctgcagttg 20

RESULT 2

AA086648/C
ID AA086648 standard; DNA; 36 BP.

XX AA086648;

DT 27-SEP-1995 (first entry)

DE Bcl-2 splice acceptor site.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;

OS Synthetic.

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

PS Disclosure; Page 13; 108pp; English.

CC The antisense oligonucleotide SA-AS (AA086647) is complementary to a
portion of the splice acceptor site of the pre-mRNA coding strand of
the human bcl-2 gene. It reduces the expression of bcl-2 gene product,
thereby inducing programmed cell death of certain cancer cells. The
corresp. bcl-2 sense splice acceptor site region was synthesized for
use as a control.

CC Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 16; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaagcctcctgcagttg 20
|||||

Db 24 ACAAGGCATCTGCGAGTTG 5

RESULT 3

AAV19656/C
ID AAV19656 standard; DNA; 36 BP.

XX AAV19656;

DT 12-JUN-1998 (first entry)

DE Human bcl-2 oligonucleotide 3.

KW Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

KW cancer; ss.

OS Synthetic.

PN Homo Sapiens.

PD US5734033-A.

PF 31-MAR-1998.

PR 24-MAR-1994; 94US-0288692.

PR 21-FEB-1992; 92US-0840716.

PR 22-DEC-1988; 88US-0288692.

PR 24-MAR-1994; 94US-0217082.

PA (TYPE-) UNIV PENNSYLVANIA.

PI Reed J;

DR WPI; 1998-229881/20.

PT Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful

PT for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

PS Disclosure; Columns 3-4; 21pp; English.

CC This is a human bcl-2 oligonucleotide based on which an antisense
oligonucleotide complementary to the splice acceptor site of the human
bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
strategic sites such as the translation initiation site, donor and
acceptor splicing sites, or sites for transportation or degradation.
Blocking translation at such strategic sites prevents the formation of a
functional bcl-2 gene product. These oligonucleotides may be used for
treating cancers associated with high levels of bcl-2 gene expression,
especially lymphomas and some leukaemias.

CC Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.5;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 acaagcctcctgcagttg 20
|||||

Db 24 ACAAGGCATCTGCGAGTTG 5

RESULT 4

AAC63894/C
ID AAC63894 standard; DNA; 40 BP.

XX AAC63894;

XX AAC63894;

PN WO200020445-A2.
 XX 13-APR-2000.
 PD
 XX
 PF 15-SEP-1999; 99WO-IB01664.
 XX
 PR 02-OCT-1998; 98US-0165863.
 PR 09-APR-1999; 99US-0289350.
 XX
 PA (CHAUV/) CHAUV P.
 PA (LUTIT/) LUTTEN R.
 PA (DEMO/) DEMOTTE N.
 PA (DEFF/) DEFOUR M.
 PA (LURON/) LURQUIN C.
 PA (TRAV/) TRAVERSARI C.
 PA (STRO/) STROOBANT V.
 PA (CORN/) CORNELIS G R.
 PA (BOON/) BOON-FALLEUR T.
 PA (VBRU/) VAN DER BRUGGEN P.
 XX
 PI Chaux P, Luiten R, Demotte N, Duffour M, Lurquin C, Traversari C;
 PI Stroobant V, Cornelis GR, Boon-Falleur T, Van Der Bruggen P;
 PI Schultz E, Warnier G;
 DR WPI: 2000-303739/26.
 XX
 XX Isolation of cytotoxic T-lymphocytes clones by successive steps of
 PT stimulation and testing of lymphocytes with antigen presenting cells
 PT which present antigens derived from different expression systems
 XX
 XX Example 1: Page 38; 99pp; English.
 XX
 CC AAA09228-35 are primers to amplify MAGE cDNA. The MAGE cDNA was linked
 CC in-frame to a sequence encoding a truncated Yope (Yope 1-130). Vectors
 CC containing this sequence were used to generate recombinant Yersina.
 CC A novel method of isolation of cytotoxic T-lymphocytes (CTL) clones
 CC comprising successive steps of stimulation and testing of lymphocytes
 CC with antigen presenting cells (APCs) which present antigens derived
 CC from different expression systems. The CTL clones isolated recognize
 CC specific antigenic peptides of proteins, preferably of the MAGE family.
 CC The APC is autologous and each expression systems is different from at
 CC least one of the other expression systems, therefore isolating a
 CC cytotoxic T cell clone specific for the protein. The method can also be
 CC used to identify an antigenic peptide epitope. Isolated CTL clones
 CC are specific for a peptide/human leukocyte antigen (HLA) complex are
 CC claimed. The CTL cells specific for the complexes, peptides or cells
 CC which present the complexes on the cell surface are useful for treating
 CC pathological conditions characterized by abnormal expression of the
 CC complexes.
 CC
 CC Sequence 30 BP; 7 A; 9 C; 7 G; 7 T; 0 other;
 XX
 SO
 Query Match 71.0%; Score 14.2; DB 21; Length 30;
 Best Local Similarity 84.2%; Pred. No. 1.1e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 2 caaagcatctcgcagtg 20
 ||| ||||| ||||| ||
 Db 3 cagagtcactctgcagatg 21

KW GTP hydrolysis; G protein activity; pheromone response pathway;
 KW G protein-coupled signal transduction; G-gamma selectivity;
 KW cellular signal transduction; FUS1 promoter; PCR primer; ss.
 XX
 XX Synthetic.
 OS Saccharomyces cerevisiae.
 OS
 PN WO9958670-A1.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-US10151.
 XX
 PR 08-MAY-1998; 98US-0084842.
 PR 07-OCT-1998; 98US-0103355.
 XX
 PA (CADU-) CADUS PHARM CORP.
 XX
 PI Cismowski M, Duzic E;
 PI WPI: 2000-072337/06.
 DR
 XX A new activator of G protein signalling used to treat disorders
 PT characterized by an aberrant AGS protein activity -
 PT
 PS Disclosure; Page 141; 162pp; English.
 XX
 CC PCR primers AA36900-01 were used to amplify the yeast FUS1 promoter
 CC sequence. The amplified fragment was used to construct host yeast
 CC strains for use in a screening assay to identify a protein which
 CC is an activator of G protein signalling (AGS protein). The AGS
 CC cDNA sequence was isolated from a human liver cDNA library. The AGS
 CC protein exhibits homology to ras-related G proteins, and contains
 CC alterations in conserved amino acids consistent with a deficiency in
 CC GTP hydrolysis activity. AGS stimulates G protein activity, G
 CC protein-coupled signal transduction and the pheromone response pathway
 CC in a receptor-independent manner. The AGS protein also shows G-gamma
 CC selectivity, as measured by growth assays in yeast expressing various
 CC mammalian G-gamma constructs, and tissue-specific expression, as
 CC measured by Northern blot analysis. The AGS protein can be used to
 CC screen for compounds that modulate cellular signal transduction. The
 CC protein is used to treat disorders characterized by an aberrant
 CC AGS protein activity or AGS nucleic acid expression.
 CC
 CC Sequence 41 BP; 8 A; 11 C; 11 G; 11 T; 0 other;
 SO
 Query Match 71.0%; Score 14.2; DB 21; Length 41;
 Best Local Similarity 84.2%; Pred. No. 1.2e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 acaagcatctcgcagtg 19
 ||| ||||| ||||| ||
 Db 36 AAAAGGCATCTGCAGAT 18

RESULT 7
 ID AA36900/c
 XX AA36900 standard; DNA; 41 BP.
 AC
 XX AA36900;
 DT 13-MAR-2000 (first entry)
 XX
 DE PCR primer used to amplify the yeast FUS1 promoter sequence.
 XX
 KW Activator of G protein signalling; AGS; ras-related G protein;

RESULT 8
 ID AAV36324/c
 XX AAV36324 standard; DNA; 45 BP.
 AC
 XX AAV36324;
 DT 12-OCT-1998 (first entry)
 XX
 DE Human GABA receptor epsilon subunit DNA probe 1.
 KW GABA receptor; gamma-amino butyric acid receptor; human;
 KW appetite; cognition; probe; ss.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9823742-A1.

XX 04-JUN-1998.
 XX 18-NOV-1997; 97WO-GB03159.
 XX 03-OCT-1997; 97GB-0020995.
 XX 25-NOV-1996; 96GB-0024442.
 XX (MERI) MERCK SHARP & DOHME LTD.
 XX Whiting PJ;
 XX WPI, 1998-322722/28.
 XX New isolated GABA receptor subunit, epsilon - used to develop
 XX products for the screening and design of drugs, e.g. for modulating
 XX appetite behaviours, hormonal interactions and cognition
 XX
 XX Example 3; Page 20; 37pp; English.
 XX Antisense oligonucleotide probes 1 and 2 (see AAV36325) are based
 XX on human GABA receptor novel epsilon subunit cDNA (see AAV36319).
 XX Each was radiolabelled at the 3' end with (35S)deoxyadenosine
 XX 5'-(thiotriphosphate) and used in in situ hybridisation assays
 XX to localise the epsilon subunit in monkey brain. The localisation
 XX appeared to be very restricted, residing mainly in the hypothalamus
 XX and arcuate nucleus. The new GABA receptor epsilon subunit (see
 XX AAV61045) can be used in the screening and design of drugs which act
 XX on the GABA receptor and which may be useful e.g. for the modulation
 XX of appetite behaviours, hormonal interactions and cognition.
 XX
 XX Sequence 45 BP; 9 A; 13 C; 11 G; 12 T; 0 other;

Query Match 68.0%; Score 13.6; DB 19; Length 45;
 Best local Similarity 80.0%; Pred. No. 2.4e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 acaaggcatctgcagttg 20
 ||||| || ||||| |||||
 DB 29 ACMAAGCTTCGTGATG 10

RESULT 9
 AAQ34907/c
 ID AAQ34907 standard; DNA; 57 BP.
 XX AAQ34907;
 XX 10-MAY-1993 (first entry)
 XX PCR primer #63 used to make LHR chimeras.
 XX Follicle stimulating hormone receptor; luteinising hormone receptor;
 XX human chorionic gonadotropin; glycoprotein hormone receptor;
 XX chimera: chimera.
 XX Chimeraic; homo sapiens.
 XX WO9222667-A.
 XX 23-DEC-1992.
 XX 12-JUN-1992; 92WO-US04987.
 XX 14-JUN-1991; 91US-0715911.
 XX (UYNE-) UNIV NEW JERSEY.
 XX Bernard M, Moyle WR, Myers R;
 XX WPI; 1993-018150/02.

PT Glyco:protein hormone receptor analogues - having binding
 PT affinity to human chorionic gonadotropin, luteinising and
 PT follicle stimulating hormones, useful in bio:immunoassays
 XX
 XX Example 34; Page 37; 103pp; English.
 XX This PCR primer was used with AAQ34908 in the construction of a
 XX vector coding for an LH receptor analogue.
 XX
 XX Sequence 57 BP; 13 A; 10 C; 19 G; 15 T; 0 other;

Query Match 68.0%; Score 13.6; DB 14; Length 57;
 Best local Similarity 80.0%; Pred. No. 2.5e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 acaaggcatctgcagttg 20
 ||||| || ||||| |||||
 DB 48 ACACGCGCATCAGCACTTG 29

RESULT 10
 AAV77691
 ID AAV77691 standard; DNA; 57 BP.
 XX AAV77691;
 XX 16-MAR-1999 (first entry)

DE Staphylococcus aureus contig SEQ ID #3380.
 XX
 XX Computer readable medium; vaccine; S.aureus infection; immunodetection;
 XX cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy;
 XX skin infection; surgical wound infection; scalded skin syndrome;
 XX toxic shock syndrome; ds.
 XX
 XX Staphylococcus aureus.
 XX
 XX EP786519-A2.
 XX 30-JUL-1997.
 XX 07-JAN-1997; 97EP-0100117.
 XX 05-JAN-1996; 96US-0009861.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA;
 XX Rosen CA;
 XX WPI; 1997-374922/35.

PT Polynucleotide(s) and proteins derived from Staphylococcus aureus
 PT stored on computer readable medium and used in the production of
 PT anti-S.aureus vaccines

Claim 1; Page 2535; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
 CC of the invention. The DNA sequences are recorded on a computer readable
 CC medium, preferably selected from a floppy or hard disk, random access
 CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using
 CC the S.aureus DNA sequences allows putative functions to be assigned so
 CC that protein-encoding or regulatory regions of commercial, therapeutic or
 CC industrial importance can be obtained. Specifically, sequences which are
 CC likely to encode antigens have been identified and these polypeptides can
 CC be used in a vaccine composition against S.aureus infection. The
 CC polypeptides can also be used in a kit for the immunodetection of
 CC S.aureus in a sample. S.aureus is implicated in numerous human diseases,
 CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,
 CC skin and surgical wound infections, scalded skin syndrome, toxic shock
 CC syndrome, etc. Organisms transformed with the DNA sequences can be used

CC for recombinant production of the polypeptides. The new DNA sequences
CC (and their fragments) are useful as primers or probes for isolating
CC homologues of any of the S.aureus DNA sequences contained on the
CC computer readable medium.

SO Sequence 57 BP; 23 A; 8 C; 10 G; 16 T; 0 other;

Query Match 68.0%; Score 13.6; DB 18; Length 57;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 acaagcattcgtcagcttg 20
1 acaagcattcgtcagcttg 20

RESULT 11

AAV69904/C
ID AAV69904 standard; DNA: 20 BP.

AC AAV69904;

DT 18-FEB-1999 (first entry)

DE PCR primer used to amplify heat-resistant maltose phosphorylase DNA.

KW Heat-resistant maltose phosphorylase; Bacillus RK-1; PCR primer; ss.

OS Synthetic.

OS Bacillus sp.

PN JP10262683-A.

PD 06-OCT-1998.

PF 25-MAR-1997; 97JP-0109996.

PR 25-MAR-1997; 97JP-0109996.

PA (SHOS) SHOMA SANGYO CO.

WPI; 1999-002482/01.

PT Nucleic acid encoding recombinant heat-resistant maltose
production of the enzyme

PS Example 1; Page 8; 27pp; Japanese.

CC PCR primers AAV69904-05 were used to amplify DNA encoding recombinant
CC heat-resistant maltose phosphorylase from Bacillus sp. RK-1 genomic
CC DNA. The enzyme reversibly phosphorylates maltose and has an optimum
CC temperature of 60-70 degrees Celsius for maltose phosphorylase.

SO Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 other;

Query Match 67.0%; Score 13.4; DB 20; Length 20;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 aaagcattcgtcag 17
1 aaagcattcgtcag 17

RESULT 12

AAAD26507/C
ID AAD26507 standard; DNA: 21 BP.

AC AAD26507;

DT 26-MAR-2002 (first entry)

DE 898001 PCR primer used to generate alpha (1, 3) GT exon 9 DNA.

KW Xenotransplantation; Gal-alpha (1,3)Gal; GAL determinant; surgery;
KW alpha(1,3) galactosyltransferase; alpha (1, 3) GT; drug screening;
KW gene therapy; PCR primer; ss.

OS Unidentified.

PN WO20018096-A2.

PD 22-NOV-2001.

PF 14-MAY-2001; 2001WO-US15765.

PR 15-MAY-2000; 2000US-204148P.

PA (GERO-) GERON CORP.

PI Denning C, Clark J;

WPI; 2002-089848/12.

PT New ovine tissue devoid of antibody-detectable Gal-alpha(1,3)Gal
determinants, for xenotransplantation, and in the treatment of the
human body by surgery or therapy

PS Example 2; Page 25; 86pp; English.

CC The patent discloses immunologically compatible animal tissue, suitable
CC for xenotransplantation into human patients. The invention also relates
CC to an ovine tissue devoid of antibody-detectable Gal-alpha (1,3)Gal (GAL)
CC determinants which are made by alpha(1,3) galactosyltransferase (GT). The
CC ovine tissue is useful for treatment of human body by surgery or therapy
CC and in xenotransplantation, by transplanting the ovine tissue into a
CC mammal having circulating antibody against Gal alpha(1,3)GT determinants.
CC Polynucleotide constructs of the invention are useful for inactivating
CC an alpha1,3 GT gene in an ovine cell. Alpha (1,3) GT sequences are useful
CC for drug screening and for the production of GAL containing synthetic
CC oligosaccharides. Sequences of the invention are also useful in gene
CC therapy. The present DNA sequence is a PCR primer which is used for
CC generating phage G alpha (1, 3) GT exon 9 DNA.

SO Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;

Query Match 67.0%; Score 13.4; DB 24; Length 21;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 caaagcattcgtcga 16
1 caaagcattcgtcga 16

RESULT 13

AAAD00976
ID AAD00976 standard; DNA: 20 BP.

AC AAD00976;

DT 21-SEP-2000 (first entry)

DE Primer #2 for TOP5 CAPS marker to map Arabidopsis thaliana PAD4 gene.

KW PAD4; disease resistance; phytoalexin; PR-1; PR-5;
KW pathogenesis-related protein; BGL2; beta-glucanase; ASA1;
KW anthranilate synthase; defence response; salicylic acid; SA;
KW signal transduction; transgenic plant; pathogen; bacteria; fungi;
KW nematode; Phytophthora; Peronospora; pseudomonas; plant; agronomy;
KW crop; chromosome 3; pad4-1; PCR primer; TOP5 CAPS marker;

KM Cleaved Amplified Polymorphic Sequence marker; ss.

XX Arabidopsis thaliana.

XX WO200029595-A1.

XX 25-MAY-2000.

PF 04-NOV-1999; 99WO-US26106.

XX 12-NOV-1998; 98US-0190733.

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

PA (PLAN-) PLANT BIOSCIENCE LTD.

PI Glazebrook J, Jirage D, Tootle T, Feys BfJ;

DR WPI: 2000-387805/33.

PT New PAD4 polypeptide from Arabidopsis thaliana, useful to enhance plant

PT resistance to diseases due to pathogens such as Phytophthora e.g. to

PT improve crop quality or yields

XX Example 2; Page 48; 181pp; English.

XX The present sequence is a primer for ROP5 Cleaved Amplified

CC Polymorphic Sequence (CAPS) marker which is used to map

CC Arabidopsis thaliana PAD4 and pad4-1 genes.

CC PAD4 gene is located on Arabidopsis chromosome 3 and encodes a

CC protein which plays an important role in disease resistance

CC in plants. The protein has positive

CC regulatory effect on phytoalexin levels and PR-1 (pathogenesis-related

CC protein) expression levels, but has no effect on PR-5 (pathogenesis-

CC related protein), BGL2 (beta-glucanase) or ASH1 (anthranilate synthase)

CC expression levels in a disease defence response by a host plant.

CC PAD4 is required upstream from salicylic acid in the signal

CC transduction pathway leading from infection to activation of defence

CC responses. It is used to produce transgenic plants which have enhanced

CC resistance to diseases caused due to pathogens such as bacteria, fungi,

CC and nematodes, especially Phytophthora, Petonospora or Pseudomonas.

CC Such transgenic plants are useful agronomically e.g. to improve crop

CC quality or yield.

CC

CC

CC

CC

CC

CC

CC

CC

Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 other;

Query Match 66.0%; Score 13.2; DB 21; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.4e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acaagcattctgact 18

DB 3 actgaagcattctgact 20

RESULT 14

ID AAC83346 standard; DNA; 30 BP.

XX AAC83346;

XX 26-FEB-2001 (first entry)

XX Primer U75329-71R.

XX Prostate specific androgen regulated protein; ARSDRI; TMPRSS2;

XX PART-1; neoplastic; ss.

XX Unidentified.

XX WO200065067-A2.

XX 02-NOV-2000.

XX 21-APR-2000; 2000WO-US10920.

XX 23-APR-1999; 99US-0130778.

XX 30-DEC-1999; 99US-0151585.

XX 30-DEC-1999; 99US-0174003.

XX 24-JAN-2000; 2000US-0177751.

XX (UNIV) UNIV WASHINGTON.

XX Nelson PS, Hood L, Lin B;

XX WPI: 2000-679676/66.

XX Polynucleotide encoding prostate specific androgen regulated

XX polypeptides and inhibitor of the peptides useful for treating or

XX reducing the progression of prostate neoplastic condition in an

XX individual

XX Example 11; Page 59; 121pp; English.

XX The present invention relates to prostate specific androgen regulated

XX proteins. The invention may be used to determine an expression level

XX of the prostate-specific proteins ARSDRI, TMPRSS2, or PART-1 in a

XX fluid sample or prostate cell sample from an individual. It may also

XX be used for diagnosing and predicting the susceptibility of a

XX prostate neoplastic condition in an individual. Inhibitors of the

XX proteins are useful for treating or preventing the progression of a

XX prostate neoplastic condition.

XX

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XX

RESULT 15

ID AAT02537 standard; DNA; 43 BP.

XX AAT02537;

XX 07-JUN-1996 (first entry)

XX Vaccinia virus ORF A8L primer oas-9t.

XX Foreign protein; vaccine; defective poxvirus; vaccinia; complementation;

XX essential region; primer; PCR; amplification; helper cell line; ss;

XX viral genome organisation; homologous recombination; expression cassette.

XX Synthetic.

XX WO9530018-A2.

XX 09-NOV-1995.

XX 28-APR-1995; 95WO-EP01629.

XX 29-APR-1994; 94US-0235392.

XX (IMMO) IMMUNO AG.

XX Dörner F, Falkner F, Holzer G;

XX WPI: 1995-393089/50.

XX Defective pox: virus lacking essential region and comprising foreign

XX

PT DNA - is only viable in presence of complementation, useful for
PT vaccines

PS Example 3; Page 21; 67pp; English.

XX The expression of foreign proteins for use as vaccines involves the
CC construction of a defective poxvirus, pref. vaccinia, in which the DNA
CC encoding the foreign protein is inserted into a deleted essential
CC region of the virus. The defective viruses are only viable by
CC complementation which is provided by an external source e.g. as a plasmid
CC such as pCMT1 contg. the required gene.
CC The primers AA02537-8 were used to amplify the vaccinia A8L open
CC reading frame (ORF) for the construction of a helper cell line contg. the
CC plasmid pSV-A8L-EDH. This plasmid contains the A8L gene (which encodes
CC the larger (82 kD) subunit of the vaccinia virus early transcription
CC factor (VETF)) under control of the SV40 promoter. It expresses the A8L
CC gene product in transfected monkey kidney Vero cells and can complement
CC the defective vaccinia virus d-A8L-2G, in which the wild type A8L gene is
CC replaced, by homologous recombination, with a defective A8L gene contg. a
CC lacZ-gpt expression cassette. The primers amplify the A8L sequence as a
CC 2.1 kb prod. which was cloned into pCMT1 to produce pCR-A8L. This
CC plasmid was subsequently used to construct pSV-A8L-EDH.

XX Sequence 43 BP; 16 A; 6 C; 10 G; 11 T; 0 other;

Query Match

65.0%; Score 13; DB 16; Length 43;

Best Local Similarity 100.0%; Pred. No. 4.7e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gcatacctgcagtt 19
|||||

DB 14 GCATCCTGCAGTT 2

Search completed: June 28, 2002, 22:40:08
Job time: 8084 sec

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:41 ; Search time 334.55 Seconds
(without alignments)
14.684 Million cell updates/sec

Title: US-09-709-170A-5

Perfect score: 20
Sequence: 1 acaagcatctgtcagttg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfileseq1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1 US-08-217-082A-5	Sequence 5, Appl1
2	20	100.0	20	2 US-08-465-485A-5	Sequence 5, Appl1
3	20	100.0	20	3 US-09-080-285-5	Sequence 5, Appl1
4	20	100.0	36	1 US-08-217-082A-6	Sequence 6, Appl1
5	20	100.0	36	2 US-08-465-485A-6	Sequence 6, Appl1
6	20	100.0	36	3 US-09-080-285-6	Sequence 6, Appl1
7	15.2	76.0	27	3 US-08-513-974B-87	Sequence 87, Appl1
8	13.8	69.0	27	3 US-08-513-974B-90	Sequence 90, Appl1
9	13.4	67.0	27	3 US-08-513-974B-89	Sequence 89, Appl1
10	13.4	67.0	30	3 US-08-513-974B-137	Sequence 137, Appl1
11	12.8	64.0	21	2 US-08-932-978-4	Sequence 4, Appl1
12	12.8	64.0	27	3 US-08-513-974B-86	Sequence 86, Appl1
13	12.8	64.0	27	3 US-08-513-974B-138	Sequence 138, Appl1
14	12.6	63.0	28	1 US-07-971-819A-30	Sequence 30, Appl1
15	12.6	63.0	28	1 US-07-977-434-26	Sequence 26, Appl1
16	12.6	63.0	28	1 US-08-475-231-30	Sequence 26, Appl1
17	12.6	63.0	28	1 US-08-458-819-26	Sequence 26, Appl1
18	12.6	63.0	28	5 PCT-US91-07035-26	Sequence 26, Appl1
19	12.6	63.0	29	4 US-09-199-290-20	Sequence 20, Appl1
20	12.6	63.0	30	4 US-08-446-935-13	Sequence 13, Appl1
21	12.6	63.0	31	4 US-08-852-001-15	Sequence 15, Appl1
22	12.6	63.0	33	1 US-08-310-416A-7	Sequence 7, Appl1
23	12.6	63.0	33	2 US-08-888-171-7	Sequence 7, Appl1
24	12.6	63.0	46	4 US-09-507-323B-4	Sequence 4, Appl1
25	12.6	63.0	60	1 US-08-424-788-15	Sequence 15, Appl1
26	12.4	62.0	29	2 US-08-560-098A-39	Sequence 39, Appl1
27	12.4	62.0	33	4 US-08-427-569-48	Sequence 48, Appl1

C 28	12.4	62.0	35	3	US-08-785-247-19	Sequence 19, Appl1
C 29	12.4	62.0	39	2	US-08-414-657D-40	Sequence 40, Appl1
C 30	12.4	62.0	40	1	US-07-854-536B-54	Sequence 54, Appl1
C 31	12.4	62.0	40	1	US-07-854-536B-55	Sequence 55, Appl1
C 32	12.4	62.0	43	2	US-08-560-098A-40	Sequence 40, Appl1
C 33	12.4	62.0	59	1	US-07-859-453E-5	Sequence 5, Appl1
C 34	12.4	62.0	59	1	US-07-859-453E-7	Sequence 7, Appl1
C 35	12.4	62.0	59	1	US-07-859-453E-9	Sequence 9, Appl1
C 36	12.4	62.0	59	1	US-07-859-453E-11	Sequence 11, Appl1
C 37	12.4	62.0	64	6	542249-11	Patent No. 542249
C 38	12.2	61.0	17	4	US-08-584-040-7778	Sequence 7778, Appl1
C 39	12.2	61.0	27	1	US-08-348-891A-19	Sequence 19, Appl1
C 40	12.2	61.0	27	1	US-08-905-817-19	Sequence 19, Appl1
C 41	12.2	61.0	27	3	US-08-513-974B-2	Sequence 2, Appl1
C 42	12.2	61.0	27	3	US-08-513-974B-76	Sequence 76, Appl1
C 43	12.2	61.0	27	4	US-08-776-971-30	Sequence 30, Appl1
C 44	12.2	61.0	33	1	US-08-299-249A-15	Sequence 15, Appl1
C 45	12.2	61.0	33	3	US-08-894-173-11	Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-08-217-082A-5
Sequence 5, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCE ADDRESSES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-5

ADDRESSEE: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-6

Query Match 100.0%; Score 20; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgcagttg 20
|||||
DB 24 ACAAGCCTCCTGCAGTTG 5

RESULT 5
US-08-465-485A-6/c
Sequence 6, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-6

Query Match 100.0%; Score 20; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 acaagcctcctgcagttg 20
|||||
DB 24 ACAAGCCTCCTGCAGTTG 5

RESULT 6
US-09-080-285-6/c
Sequence 6, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-6

Query Match 100.0%; Score 20; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 acaagcctcctgcagtgtg 20
Db 24 ACAAGCCTCCTGCAGTGTG 5

RESULT 7
US-08-513-974B-87/C
Sequence 87, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: GDNA
US-08-513-974B-87

Query Match 76.0%; Score 15.2; DB 3; Length 27;
Best Local Similarity 85.0%; Pred. No. 67;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 acaagcctcctgcagtgtg 20
Db 25 ACAAGCCTCCTGCAGTGTG 6

RESULT 8
US-08-513-974B-90/C
Sequence 90, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536

RESULT 10
US-08-513-974B-137/C
; Sequence 137, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhito
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 137:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-513-974B-137

Query Match 67.0%; Score 13.4; DB 3; Length 30;
Best Local Similarity 93.3%; Pred. No. 5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 aaagcctcctcgag 17
|||||
DB 23 AAAGCATCAGACAG 9

RESULT 11
US-08-932-978-4
; Sequence 4, Application US/08932978
; Patent No. 5885804
; GENERAL INFORMATION:
; APPLICANT: Zalacain, Magdalena
; APPLICANT: Brown, James R.
; TITLE OF INVENTION: NOVEL PHO
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/932,978
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dickinson, Todd O
; REGISTRATION NUMBER: 28,354
; REFERENCE/DOCKET NUMBER: GM0100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2252
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-932-978-4

Query Match 64.0%; Score 12.8; DB 2; Length 21;
Best Local Similarity 87.5%; Pred. No. 9.3e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 acaagcctcctgca 16
|||||
DB 1 ACAAGCATCAGTCA 16

RESULT 12

US-08-513-974B-86/C
Sequence 86 Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-513-974B-86
Query Match 64.0%; Score 12.8; DB 3; Length 27;
Best local Similarity 87.5%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 25 ACAAGGACAGCCAGCA 10
OY 1 acaaggacatcctgca 16
|||||
Db 25 ACAAGGACAGCCAGCA 10
RESULT 13
US-08-513-974B-138/C
Sequence 138 Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ. ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-513-97AB-138

Query Match 64.0%; Score 12.8; DB 3; Length 30;
Best local similarity 87.5%; Pred. No. 9.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 acaaggatctctgca 16
|||||||
DB 25 ACAAGGACGCCAGCA 10

RESULT 14
US-07-971-819A-30
Sequence 30, Application US/07971819A
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Scofield, Suzanne C.
TITLE OF INVENTION: Purified Thermostable Nucleic Acid
TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: USA
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/971,819A
FILING DATE: 19930203
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stacey R. Sias, Ph.D.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2863
TELEFAX: (510) 814-2977
TELEX:
INFORMATION FOR SEQ. ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other Nucleic Acid

US-07-971-819A-30

Query Match 63.0%; Score 12.6; DB 1; Length 28;
Best local similarity 78.9%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

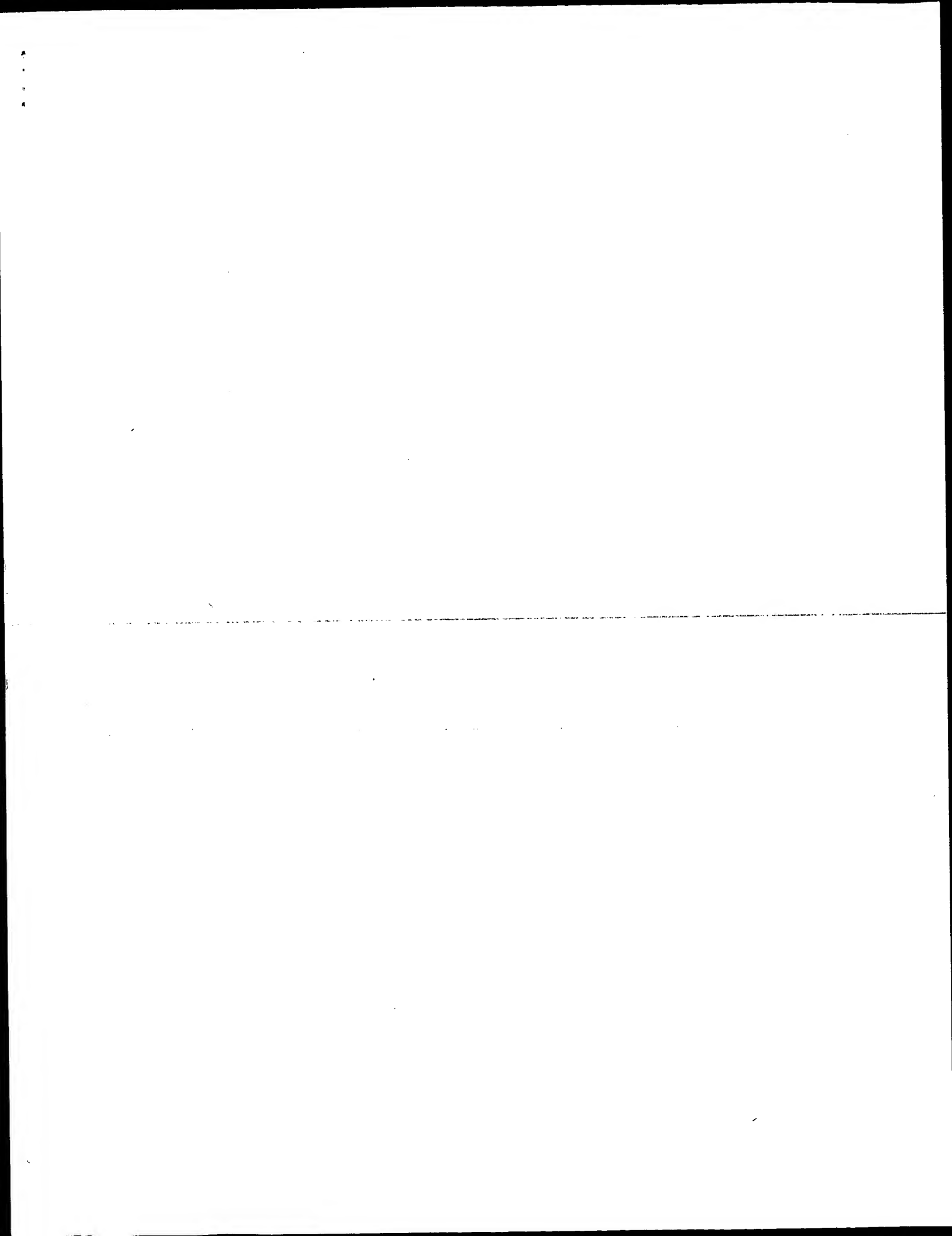
OY 1 acaaggatctctgcagt 19
|||||||
DB 2 ATAAAGCATGCTTCAGCT 20

RESULT 15
US-07-977-434-26
Sequence 26, Application US/07977434
Patent No. 546591
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: 7
SOFTWARE: WordPerfect 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/977,434
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 557,517
 FILING DATE: 24-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Luann Cseert
 REGISTRATION NUMBER: 31,922
 REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2972
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA primer FL63
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-07-977-434-26

Query Match 63.0%; Score 12.6; DB 1; Length 28;
 Best local Similarity 78.9%; Pred No. 1.2e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 acaagagcatcctgcagtt 19
 1 ||||| 11111
 Db 2 ATAAGCATGCTTCAGCT 20

Search completed: June 28, 2002, 22:16:43
 Job time: 8269 sec



Mon Jul 1 08:40:57 2002

us-09-709-170a-6.szlm75.rge

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:10:56 ; Search time 3762.88 Seconds
(without alignments)
200.207 Million cell updates/sec

US-09-709-170A-6

Title: 36
Perfect score: 1
Sequence: 1 ccccccaatgcagatgccttctgtgaactgacg 36

Scoring table: IDENTITY-NDC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1: *
1: gb_da: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pt: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_hlg_hum: *
31: em_hlg_inv: *
32: em_hlg_other: *
33: em_hlg_inv: *

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

1	36	100.0	36	6	AR052608	Sequence 6
2	36	100.0	36	6	196087	Sequence 6
3	24	66.7	34	6	AR007302	Sequence 6
4	20	55.6	20	6	AR052607	Sequence 5
5	20	55.6	20	6	196086	Sequence 5
6	16.8	46.7	51	6	AX163121	Sequence 5
7	16.8	46.7	51	6	AX163122	Sequence 5
8	16.8	46.7	51	6	AX163123	Sequence 5
9	15.8	43.9	42	9	568042	Sequence 5
10	15.8	43.9	57	9	HSTCR021	Sequence 5
11	15.8	43.9	66	9	HSTCR021	Sequence 5
12	15.6	43.3	31	6	AX354576	Sequence 5
13	15.4	42.8	30	6	AR178017	Sequence 5
14	15.4	42.8	31	6	AR178018	Sequence 5
15	15.4	42.8	32	6	AR178019	Sequence 5
16	15.4	42.8	35	6	AX08115	Sequence 5
17	15.4	42.8	45	6	AX08115	Sequence 5
18	15.4	42.8	51	6	AX204481	Sequence 5
19	15.2	42.2	20	6	AR121062	Sequence 5
20	15.2	42.2	20	6	AR124985	Sequence 5
21	15.2	42.2	23	6	AX060729	Sequence 5
22	15.2	42.2	23	6	AX060729	Sequence 5
23	15.2	42.2	23	6	AX060908	Sequence 5
24	15.2	42.2	27	6	AR109663	Sequence 5
25	15.2	42.2	30	6	AR178033	Sequence 5
26	15.2	42.2	40	6	AR053595	Sequence 5
27	15.2	42.2	45	6	AX180787	Sequence 5
28	15.2	42.2	60	6	AR068214	Sequence 5
29	15.2	42.2	60	6	AR076966	Sequence 5
30	15.2	42.2	60	6	AR078799	Sequence 5
31	15.2	42.2	60	6	AX136804	Sequence 5
32	15.2	42.2	60	6	E41200	Sequence 5
33	15.2	42.2	60	6	E41216	Sequence 5
34	15.2	42.2	60	6	E5308	Sequence 5
35	15.2	42.2	60	6	E64583	Sequence 5
36	15.2	42.2	60	9	HSAD2517	Sequence 5
37	15.2	42.2	61	6	AX127334	Sequence 5
38	15.2	42.2	63	6	AR109475	Sequence 5
39	15.2	42.2	63	6	E16172	Sequence 5
40	15.2	42.2	70	6	AX249578	Sequence 5
41	15.2	42.2	31	6	AX249578	Sequence 5
42	15.2	42.2	49	6	AR164215	Sequence 5
43	15.2	42.2	51	6	AX161217	Sequence 5
44	15.2	42.2	51	6	AX161219	Sequence 5
45	15.2	42.2	54	6	AR050475	Sequence 5

ALIGNMENTS

RESULT 1	AR052608	36 bp	DNA	1 linear	PAT 29-SEP-1999
LOCUS	AR052608	6 from patent US 5831066.			
DEFINITION	Sequence 6				
ACCESSION	AR052608				
VERSION	AR052608.1	GI:5975972			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 36)				
AUTHORS	Reed, J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A 6/03-NOV-1998;				
FEATURES	Location/Qualifiers				
SOURCE	1..36				
BASE COUNT	7 a 11 c 10 g 8 t				
ORIGIN					

Query Match 100.0%; Score 36; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccccaactgcagatgcttctgtgaactgacg 36
Db 1 ccccaactgcagatgcttctgtgaactgacg 36

RESULT 2
LOCUS 196087
DEFINITION Sequence 6 from patent US 5734033.
ACCESSION 196087
VERSION 196087.1 GI:3940557
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 6 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..36
BASE COUNT 7 a 11 c 10 g 8 t
ORIGIN

Query Match 100.0%; Score 36; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccccaactgcagatgcttctgtgaactgacg 36
Db 1 ccccaactgcagatgcttctgtgaactgacg 36

RESULT 3
LOCUS AR007302
DEFINITION Sequence 16 from patent US 5750390.
ACCESSION AR007302
VERSION AR007302.1 GI:3966786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Thompson,J.D. and Draper,K.G.
TITLE Method and reagent for treatment of diseases caused by expression of the bcl-2 gene
JOURNAL Patent: US 5750390-A 16 12-MAY-1998;
FEATURES Location/Qualifiers
source 1..34
BASE COUNT 6 a 9 c 11 g 8 t
ORIGIN

Query Match 66.7%; Score 24; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 ggaatgccttggaactgacg 36
Db 1 ggaatgccttggaactgacg 24

RESULT 4
LOCUS AR052607
DEFINITION Sequence 5 from patent US 5831066.
ACCESSION AR052607

VERSION AR052607.1 GI:5975971
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 5 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 6 a 5 c 5 g 4 t
ORIGIN

Query Match 55.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 caactgcagatgcttctgt 24
Db 20 caactgcagatgcttctgt 1

RESULT 5
LOCUS 196086
DEFINITION Sequence 5 from patent US 5734033.
ACCESSION 196086
VERSION 196086.1 GI:3940556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 5 31-MAR-1998;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 6 a 5 c 5 g 4 t
ORIGIN

Query Match 55.6%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 caactgcagatgcttctgt 24
Db 20 caactgcagatgcttctgt 1

RESULT 6
LOCUS AX163121
DEFINITION Sequence 6449 from Patent WO0140521.
ACCESSION AX163121
VERSION AX163121.1 GI:14544452
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 51)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Shinkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 6449 07-JUN-2001;
FEATURES Location/Qualifiers

source 1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26
/note="1 of 2 allelic variants (6450 is other entry)
Accession number c927837466"

BASE COUNT 10 a 18 c 12 g 11 t

ORIGIN

Query Match 46.7%; Score 16.8; DB 6; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ccccaactgcagatgccttctggaactgtacg 36
||| ||||| ||| ||||| ||| ||| |||
10 CCACCACTGCTCGACCTTTGACGACCTCGTCGG 45

RESULT 7
AX163122 51 bp DNA linear PAT 22-JUN-2001
LOCUS AX163122 6450 from Patent WO0140521.
DEFINITION Sequence
ACCESSION AX163122
VERSION AX163122.1 GI:14544453
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shinkens, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6450 07-JUN-2001;
Curegen Corporation (US)
FEATURES
Location/Qualifiers
source 1. .51
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 26
/note="2 of 2 allelic variants (6449 is other entry)
Accession number c927837466"

BASE COUNT 10 a 19 c 12 g 10 t

ORIGIN

Query Match 46.7%; Score 16.8; DB 6; Length 51;
Best Local Similarity 66.7%; Pred. No. 1.7e+04;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 ccccaactgcagatgccttctggaactgtacg 36
||| ||||| ||| ||||| ||| ||| |||
10 CCACCACTGCTCGACCTTTGACGACCTCGTCGG 45

Db 10 CCACCACTGCTCGACCTTTGACGACCTCGTCGG 45

RESULT 8
ASYPIGR6/c 60 bp DNA linear VRT 06-MAR-1995
LOCUS ASYPIGR6 fasciatus red visual pigment gene (R007), exon 6.
DEFINITION M38630
ACCESSION M38630.1 GI:210992
VERSION M38630.1 GI:210992
KEYWORDS visual pigment.
SEGMENT 6 of 6
SOURCE Aslyanax fasciatus DNA, clone lambda R007.
ORGANISM Aslyanax mexicanus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Characiformes; Characidae; Tetraodonidae; Aslyanax.
REFERENCE 1 (bases 1 to 60)
AUTHORS Yokoyama, R. and Yokoyama, S.
TITLE Convergent evolution of the red- and green-like visual pigment
genes in fish, Aslyanax fasciatus, and human

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9315-9318 (1990)
MEDLINE 91067696
COMMENT Draft entry and computer-readable sequence for [Proc. Natl. Acad.
Sci. U.S.A. (1990) in press] kindly submitted
by S. Yokoyama, 18-SEP-1990.
Draft entry and computer-readable sequence for [Proc. Natl. Acad.
Sci. U.S.A. (1990) in press] kindly submitted
by S. Yokoyama, 18-SEP-1990.
Location/Qualifiers

FEATURES
source 1. .60
/organism="Aslyanax mexicanus"
/db_xref="taxon:7994"
/clone="lambda-007"
join(M38625.1:1..103,M38626.1:11..307,M38627.1:11..179,
M38628.1:11..176,M38629.1:11..250,11..60)
/partial
/gene="R007"
/codon_start=1
/product="red visual pigment"
/protein_id="AA62672.1"
/db_xref="GI:210994"
translation="MGDQMGDAFEAARRGDDTTRAEFTYNSNTKDPFEGPVYH
APRWVLDATCMFEVYVASTYNGLYVASAKFKLRRLHMLIVNLIAIALLETL
ASTISVNOFFGYFTLGHMPCVEGFVATCGIAGLMSLFVISMERYVYCKPQNVK
FDGRMATAGIVFTWVMSAVWCAPRIFGWSRYPHGLKTSQGVDSGSDPGVOSTMI
VLMTTCFPIPLGITLILCYIAVMMARIVVAGQODSDSTQAEKESRMVVMIMAYCE
CMGPYTFEACFAANPGYAFHPPLAAMPVAFSAATITVNPVIVFPMNRQFRVCIQOLF
GKRYDGS"

gene join(M38626.1:1..317,M38627.1:1..189,M38628.1:1..186,
M38629.1:1..260,1..60)
/gene="R007"
order(M38629.1:251..260,1..10)
/gene="R007"

INTRON /note="814 bp gap"

BASE COUNT 12 a 11 c 19 g 18 t

ORIGIN

Query Match 46.7%; Score 16.8; DB 5; Length 60;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 21; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 aactgcagatgccttctggaactgtacg 33
||| ||||| ||| ||||| ||| ||| |||
33 AGCTGCATGATGCATACGCGAAGCTGCA 6

Db 33 AGCTGCATGATGCATACGCGAAGCTGCA 6

RESULT 9
S68042 42 bp DNA linear PRI 07-MAY-1993
LOCUS S68042 hemoglobin beta chain [human, Genomic Mutant, 42 nt].
DEFINITION S68042
ACCESSION S68042.1 GI:239717
VERSION S68042.1 GI:239717
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 42)
AUTHORS Oner R., Oner, C., Wilson, J.B., Tamagnini, G.P., Ribeiro, L.M. and
Huisman, J.H.
TITLE Dominant beta-thalassemia trait in a Portuguese family is caused
by a deletion of (G)TGGTGGT(G) and an insertion of (G)GCG(G) in
codons 134, 135, 136 and 137 of the beta-globin gene
JOURNAL Br. J. Haematol. 79 (2), 306-310 (1991)
MEDLINE 92068764
COMMENT GenBank staff at the National Library of Medicine created this
entry [NCBI g1dbsg 68042] from the original journal article.
This sequence comes from Fig.2.
deletion of TG.GCT.GGT.GT at codons 134-137 (Val.Ala.Gly.Val) and
the insertion of GC.AG (Gly.Arg).
Location/Qualifiers
1. .42

gene
 /db_xref="taxon:9606"
 1..42
 /partial
 /gene="hemoglobin beta chain, beta-globin"
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 /note="This sequence comes from Fig.2; beta-globin"
 /codon_start=1
 /product="hemoglobin beta chain"
 /protein_id="AAB204A0.1"
 /db_xref="GI:239718"
 /translation="PPVQAAYQXVGRAN"
 11 a 11 c 13 g 7 t

Query Match 43.9%; Score 15.8; DB 9; Length 42;
 Best Local Similarity 65.7%; Pred. No. 4.6e+04;
 Matches 23; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2 ccccaactgcagatgccttcttggaactgtacg 36
 11 | | | | | | | | | | | | | | | | | | | | | |
 Db 1 CCACCAGTCAGAGTCCTTCAGAAAGTGGCAG 35

RESULT 10
 HSTCRA021/c 57 bp mRNA linear PRI 10-NOV-1994
 LOCUS Human mRNA for T cell receptor J alpha gene segment IGRJAL2.
 DEFINITION X58759
 ACCESSION X58759
 VERSION X58759.1 GI:36855
 KEYWORDS J-alpha gene segment; T-cell receptor alpha-chain; variable region.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 57)
 Roman-Roman, S., Ferradini, L., Azocar, J., Genevee, C., Hercend, T. and
 Triebel, F.
 Studies on the human T cell receptor alpha/beta variable region
 genes. I. Identification of 7 additional V alpha subfamilies and 14
 J alpha gene segments
 Eur. J. Immunol. 21 (4), 927-933 (1991)
 91209401
 2 (bases 1 to 57)
 Triebel, F.
 Direct Submission
 Submitted (04-JUN-1991) Triebel, F., INSERM U333, Institute
 Desmoulin, 94805 Villejuif, Cedex, France
 See also X58736-X58740, X58744-X58769.
 location/Qualifiers
 1..57
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="T lymphocytes"
 /clone="IGRJAL2"

COMMENT
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="T lymphocytes"
 /clone="IGRJAL2"

BASE COUNT 12 a 19 c 13 g 12 t 1 others
 ORIGIN

Query Match 43.9%; Score 15.8; DB 9; Length 57;
 Best Local Similarity 74.1%; Pred. No. 4.6e+04;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4 ccaactgcagatgccttcttggaact 30
 11 | | | | | | | | | | | | | | | | | | | | | |
 Db 50 CCACAGCAGAGTCCTTCGCGAGT 24

RESULT 11

HUMTCRAJL/c HUMTCRAJL 66 bp mRNA linear PRI 13-JAN-1995
 LOCUS Human rearranged T-cell receptor alpha-chain joining region (TCRA)
 DEFINITION
 ACCESSION L06877
 VERSION L06877.1 GI:339322
 KEYWORDS J-region; T-cell receptor; alpha-chain.
 SOURCE Homo sapiens (individual isolate Ja.n8) blood cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 66)
 Santamaria, P., Lewis, C. and Barbosa, J.J.
 Amino acid sequences of seven V beta, eight V alpha, and thirteen J
 alpha novel human TCR genes
 Immunogenetics 38 (2), 163 (1993)
 93246301
 location/Qualifiers
 1..66
 /organism="Homo sapiens"
 /isolate="Ja.n8"
 /db_xref="taxon:9606"
 /map="14q11.2"
 /cell_type="T-cell"
 /tissue_type="blood"
 1..66
 /gene="TCRA"
 /standard_name="J_region"
 /note="G00-120-404"
 /product="T-cell receptor alpha"
 1..66
 /gene="TCRA"
 /note="G00-120-404"
 /product="T-cell receptor alpha"
 1..66
 /gene="TCRA"
 /note="G00-120-404"
 /product="T-cell receptor alpha"
 15 a 23 c 14 g 14 t

mat_peptide

gene

J-segment

BASE COUNT 15 a 23 c 14 g 14 t
 ORIGIN

Query Match 43.9%; Score 15.8; DB 9; Length 66;
 Best Local Similarity 74.1%; Pred. No. 4.6e+04;
 Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4 ccaactgcagatgccttcttggaact 30
 11 | | | | | | | | | | | | | | | | | | | | | |
 Db 58 CCACAGCAGAGTCCTTCGCGAGT 32

RESULT 12
 AX354576/c 31 bp DNA linear PAT 06-FEB-2002
 LOCUS Sequence 23 from Patent WO0179555.
 DEFINITION AX354576
 ACCESSION AX354576
 VERSION AX354576.1 GI:18619378
 KEYWORDS
 SOURCE
 ORGANISM
 SYNTHETIC CONSTRUCT.
 SYNTHETIC CONSTRUCT.
 ARTIFICIAL SEQUENCE.
 1 (sites)
 HANCOCK, W.W. and OZKAYNAK, E.
 Roles of 14k/stat family members in tolerance induction
 Patent: WO 0179555-A 23 25-OCT-2001;
 Millennium Pharmaceuticals, Inc. (US)
 location/Qualifiers
 1..31
 /organism="Synthetic construct"
 /db_xref="taxon:32630"
 /note="antisense molecule"
 5 a 11 c 7 g 8 t

BASE COUNT 5 a 11 c 7 g 8 t
 ORIGIN

Query Match 43.3%; Score 15.6; DB 6; Length 31;
 Best Local Similarity 81.8%; Pred. No. 5.5e+04;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 8 ctgcagatgcttcttggaac 29
 ||||| |||||
 DB 25 CAGCAGATGGCTCAGTGAAC 4

RESULT 13
 LOCUS AR178017/c 30 bp DNA linear PAT 18-DEC-2001
 DEFINITION Sequence 4 from patent US 6315995.
 ACCESSION AR178017
 VERSION AR178017.1 GI:17920910

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Pinsky,D.J., Stern,D., Schmidt,A.Marie., Rose,E. and Solomon,R.A.
 TITLE Methods for treating an ischemic disorder and improving stroke outcome

JOURNAL Patent: US 6315995-A 4 13-NOV-2001;
 FEATURES location/Qualifiers
 source 1..30 /organism="unknown"

BASE COUNT 4 a 10 c 6 g 7 t 3 others
 ORIGIN

Query Match 42.8%; Score 15.4; DB 6; Length 30;
 Best Local Similarity 67.9%; Pred. No. 6.8e+04;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 7 actgcagatgcttcttggaactgtac 34
 ||||| |||||
 DB 28 ACCCCAGGGGNNNTAGAGAACTGTAC 1

RESULT 14
 LOCUS AR178018 31 bp DNA linear PAT 18-DEC-2001
 DEFINITION Sequence 5 from patent US 6315995.
 ACCESSION AR178018
 VERSION AR178018.1 GI:17920911

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 31)
 AUTHORS Pinsky,D.J., Stern,D., Schmidt,A.Marie., Rose,E. and Solomon,R.A.
 TITLE Methods for treating an ischemic disorder and improving stroke outcome

JOURNAL Patent: US 6315995-A 5 13-NOV-2001;
 FEATURES location/Qualifiers
 source 1..31 /organism="unknown"

BASE COUNT 5 a 10 c 6 g 7 t 3 others
 ORIGIN

Query Match 42.8%; Score 15.4; DB 6; Length 31;
 Best Local Similarity 67.9%; Pred. No. 6.8e+04;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 7 actgcagatgcttcttggaactgtac 34
 ||||| |||||
 DB 28 ACCCCAGGGGNNNTAGAGAACTGTAC 1

RESULT 15
 AR178019/c

LOCUS AR178019 32 bp DNA linear PAT 18-DEC-2001
 DEFINITION Sequence 6 from patent US 6315995.
 ACCESSION AR178019
 VERSION AR178019.1 GI:17920912

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 32)
 AUTHORS Pinsky,D.J., Stern,D., Schmidt,A.Marie., Rose,E. and Solomon,R.A.
 TITLE Methods for treating an ischemic disorder and improving stroke outcome

JOURNAL Patent: US 6315995-A 6 13-NOV-2001;
 FEATURES location/Qualifiers
 source 1..32 /organism="unknown"

BASE COUNT 6 a 10 c 6 g 7 t 3 others
 ORIGIN

Query Match 42.8%; Score 15.4; DB 6; Length 32;
 Best Local Similarity 67.9%; Pred. No. 6.8e+04;
 Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 7 actgcagatgcttcttggaactgtac 34
 ||||| |||||
 DB 28 ACCCCAGGGGNNNTAGAGAACTGTAC 1

Search completed: June 28, 2002, 22:11:01
 Job time: 8352 sec

Mon Jul 1 08:40:57 2002

us-09-709-170a-6.szlm75.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:08 ; Search time 1381.16 Seconds

(without alignments)
44.751 Million cell updates/sec

Title: US-09-709-170A-6

Perfect score: 36

Sequence: 1 cccccacatgcagatgcttcttgtaactgtacg 36

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_032802:*

- 1: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1995.DAT:*
- 17: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1996.DAT:*
- 18: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	16	AA086648
2	36	100.0	36	19	AAV19656
3	24	66.7	34	14	AA051962
4	20	55.6	20	19	AAV19655
5	17.2	47.8	20	21	AA65053
6	17	47.2	45	19	AAV36324
7	16.8	46.7	51	22	AAI79508
8	16.8	46.7	51	22	AAI79509
9	16.6	46.1	47	21	AA72693

10	16.2	45.0	40	21	AA638894	Chinese hamster/ra
11	16	44.4	20	21	AA237381	PCR primer for hum
12	15.8	43.9	34	17	AA714539	EC receptor PCR pr
13	15.8	43.9	36	10	AAW90551	Tissue plasminogen
14	15.8	43.9	43	22	AA690375	pC4fc:MEH1 PCR pr
15	15.6	43.3	31	24	AAAD2417	Human Stat3 antis
16	15.6	43.3	41	21	AA236900	PCR primer used to
17	15.4	42.8	31	22	AA731169	Human single nucle
18	15.4	42.8	51	22	AA799972	Human DNA containi
19	15.2	42.2	20	21	AA693232	Mouse STAT3 phosph
20	15.2	42.2	20	21	AA693647	Antisense oligonuc
21	15.2	42.2	20	22	AA515196	Human bcl-x antis
22	15.2	42.2	20	22	AA527692	Human bcl-x antis
23	15.2	42.2	20	24	AA596849	Mouse STAT3 antis
24	15.2	42.2	23	22	AA24693	PCR primer used to
25	15.2	42.2	23	22	AA724715	PCR primer used to
26	15.2	42.2	40	17	AA694418	Plasmid p1825f1 c
27	15.2	42.2	40	20	AA694418	Circular plasmid e
28	15.2	42.2	43	22	AA688841	pF1ag-CMV-5a:MEH1
29	15.2	42.2	45	22	AA690373	Human IL-17E hybri
30	15.2	42.2	51	22	AA633347	Human SNP oligonuc
31	15.2	42.2	60	17	AA742998	Fusion junction fo
32	15.2	42.2	60	21	AA694476	Vector pBR322 Scat
33	15.2	42.2	60	21	AA689951	pBR322 oligonucleo
34	15.2	42.2	60	21	AA689952	pBR322 oligonucleo
35	15.2	42.2	60	22	AA624270	Reca ligation meth
36	15.2	42.2	60	22	AA629102	Oligonucleotide 1
37	15.2	42.2	60	22	AA629118	Oligonucleotide 17
38	15.2	42.2	61	22	AA508375	Pig PHEPX 3' UTR o
39	15.2	42.2	63	19	AAV34628	Hair pin-like stru
40	15.2	42.2	75	20	AA628151	Universal adaptor
41	15	41.7	25	22	AA626064	Human PPT-1 gene e
42	15	41.7	49	16	AA63075	Primer 1 for ampli
43	15	41.7	51	22	AA631737	Human SNP oligonuc
44	15	41.7	51	22	AA6317604	Human silent SNP c
45	15	41.7	51	22	AA6317606	Human silent SNP c

ALIGNMENTS

RESULT 1	AA086648	standard; DNA; 36 BP.
ID	AA086648	
XX	AA086648	
AC	AA086648	
XX	AA086648	
DT	27-SEP-1995	(first entry)
XX	27-SEP-1995	
DE	Bcl-2 splice acceptor site.	
XX	Bcl-2 splice acceptor site.	
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;	
KW	Leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;	
ss.	ss.	
OS	Synthetic.	
XX	Synthetic.	
PN	WO9508350-A.	
PD	30-MAR-1995.	
XX	30-MAR-1995.	
PF	20-SEP-1994;	94WO-US10725.
XX	20-SEP-1994;	
PR	20-SEP-1993;	93US-0124256.
XX	20-SEP-1993;	
PA	(REED/) REED J C.	
XX	(REED/) REED J C.	
PI	Reed JC;	
XX	Reed JC;	
DR	WPI; 1995-139394/18.	
XX	WPI; 1995-139394/18.	
PT	Anti-code oligomers which bind to bcl-2 mRNA - for the treatment	
PT	of human solid tumours, esp. breast cancer	

XX PS Disclosure; Page 13; 108pp; English.
 CC CC The antisense oligonucleotide SA-AS (AA086647) is complementary to a
 CC portion of the splice acceptor site of the pre-mRNA coding strand of
 CC the human bcl-2 gene. It reduces the expression of bcl-2 gene product,
 CC thereby inducing programmed cell death of certain cancer cells. The
 CC corresp. bcl-2 sense splice acceptor site region was synthesized for
 CC use as a control.
 XX XX

Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 36; DB 16; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccccaactgcagagatgcttctgtgaactgtacg 36
 Db 1 ccccaactgcagagatgcttctgtgaactgtacg 36

RESULT 2

AAV19656 standard; DNA; 36 BP.

AAV19656;

12-JUN-1998 (first entry)

Human bcl-2 oligonucleotide 3.

Antisense oligonucleotide; bcl-2 gene; lymphoma; leukaemia; human;

cancer; ss.

Synthetic.

Homo sapiens.

US5734033-A.

31-MAR-1998.

24-MAR-1994; 94US-0288692.

21-FEB-1992; 92US-0840716.

22-DEC-1988; 88US-0288692.

24-MAR-1994; 94US-0217082.

(UYPE-) UNTV PENNSYLVANIA.

Reed J;

WPI; 1998-229881/20.

Anti-sense oligo:nucleotide(s) complementary to BCL-2 mRNA - useful
 for treating cancers, e.g. lymphoma(s) and some leukaemia(s)

Disclosure; Columns 3-4; 21pp; English.

XX XX This is a human bcl-2 oligonucleotide based on which an antisense
 CC oligonucleotide complementary to the splice acceptor site of the human
 CC bcl-2 mRNA can be constructed. Bcl-2 antisense oligonucleotides straddle
 CC strategic sites such as the translation initiation site, donor and
 CC acceptor splicing sites, or sites for transportation or degradation.
 CC Blocking translation at such strategic sites prevents the formation of a
 CC functional bcl-2 gene product. These oligonucleotides may be used for
 CC treating cancers associated with high levels of bcl-2 gene expression,
 CC especially lymphomas and some leukaemias.
 XX XX

Sequence 36 BP; 7 A; 11 C; 10 G; 8 T; 0 other;

Query Match 100.0%; Score 36; DB 19; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ccccaactgcagagatgcttctgtgaactgtacg 36
 Db 1 ccccaactgcagagatgcttctgtgaactgtacg 36

RESULT 3

AA051962 standard; RNA; 34 BP.

AA051962;

26-MAY-1994 (first entry)

BCL-2 mRNA ribozyme cleavable nucleotide (2043).

Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
 resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
 actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
 adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
 human; chronic myelogenous leukemia; CMV; follicular lymphoma;
 B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
 neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
 hairpin; hepatitis delta virus; group I intron; RNaseP, ss.

Homo sapiens.

WO9323057-A.

25-NOV-1993.

13-MAY-1993; 93WO-US04573.

14-MAY-1992; 92US-0882822.

14-MAY-1992; 92US-0882885.

26-AUG-1992; 92US-0936110.

26-AUG-1992; 92US-0936421.

26-AUG-1992; 92US-0936422.

26-AUG-1992; 92US-0936531.

26-AUG-1992; 92US-0936532.

07-DEC-1992; 92US-0987131.

19-JAN-1993; 93US-0006122.

19-JAN-1993; 93US-0008910.

(RIBO-) RIBOZYME PHARM INC.

Draper KG, Thompson JD;

WPI; 1993-386203/48.

New enzymatic RNA molecules (ribozymes), - which cleave mRNA
 associated with tumours or mRNA expressed from gene encoding
 multiple drug resistance

Claim 3; Fig 6; 69pp; English.

XX XX The sequences given in AA051825-2266 represent areas of mRNAs which are
 CC associated with development or maintenance of chronic myelogenous
 CC leukemia (CM), promyelocytic leukemia, Burkitt's lymphoma, or
 CC acute lymphocytic leukemia, follicular lymphoma, B-cell acute
 CC lymphocytic leukemia, breast cancer, colon carcinoma, neuroblastoma
 CC and lung cancer. The full length mRNAs containing these target
 CC sequences, encode aberrant cellular proteins which are able to control
 CC cellular proliferation and are directly linked to a leukemic
 CC phenotype. These target sequences are identified by the ribozyme of
 CC the invention. The ribozymes is formed in a hammerhead motif, but may
 CC also be formed in the motif of a hairpin, hepatitis delta virus, group
 CC I intron or RNaseP-like RNA. These ribozymes may be used to inhibit
 CC the development or expression of a transformed phenotype in man and
 CC other animals by modulating expression of the corresponding gene.
 CC Cleavage of target mRNAs expressed in pre-neoplastic and transformed

OS Synthetic.
OS Homo sapiens.
XX
XX WO9823742-A1.
XX
XX
PD 04-JUN-1998.
XX
XX
PF 18-NOV-1997; 97WO-GB03159.
XX
XX 03-OCT-1997; 97GB-0020995.
PR 25-NOV-1996; 96GB-0024442.
XX
XX (MERRI) MERCK SHARP & DOHME LTD.
PA
PI Whiting PJ;
XX WPI; 1998-322722/28.
XX
XX
PT New isolated GABA receptor subunit, epsilon - used to develop
PT products for the screening and design of drugs, e.g. for modulating
PT appetite behaviours, hormonal interactions and cognition
XX
XX Example 3; Page 20; 37pp; English.
XX
CC Antisense oligonucleotide probes 1 and 2 (see AAV36325) are based
CC on human GABA receptor novel epsilon subunit cDNA (see AAV36319).
CC Each was radiolabelled at the 3' end with (35S)deoxyadenosine
CC 5'-(thiotriphosphate) and used in in situ hybridisation assays
CC to localise the epsilon subunit in monkey brain. The localisation
CC appeared to be very restricted, residing mainly in the hypothalamus
CC and arcuate nucleus. The new GABA receptor epsilon subunit (see
CC AAW61045) can be used in the screening and design of drugs which act
CC on the GABA receptor and which may be useful e.g. for the modulation
CC of appetite behaviours, hormonal interactions and cognition.
XX
SQ Sequence 45 BP; 9 A; 13 C; 11 G; 12 T; 0 other;

Query Match 47.2%; Score 17; DB 19; Length 45;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 cccccaactgcagatgacttgctg 25
DB 6 ccgcacaactgcagatgacttgctg 30

RESULT 7
AAI79508
ID AAI79508 standard; DNA; 51 BP.
XX
XX AAI79508;
AC
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6449.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
XX WO200140521-A2.
PN
XX
PD 07-JUN-2001.
XX
XX
PF 30-NOV-2000; 2000MO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
PA

XX
PI Shinkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
DR
XX
XX
PT Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX
XX
PS Claim 1; Page 2481; 2653pp; English.
XX
CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AAM53114 to AAM53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 51 BP; 10 A; 18 C; 12 G; 11 T; 0 other;

Query Match 46.7%; Score 16.8; DB 22; Length 51;
Best Local Similarity 66.7%; Pred. NO. 1.4e+03;
Matches 24; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 cccccaactgcagatgacttgatgactg 36
DB 10 ccaccaactgcagatgacttgatgactg 45

RESULT 8
AAI79509
ID AAI79509 standard; DNA; 51 BP.
XX
XX AAI79509;
AC
XX
DT 09-NOV-2001 (first entry)
XX
DE Human silent SNP containing nucleic acid SEQ:6450.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
KW protein therapy; vaccine; probe; diagnostic assay; detection;
KW quantitation; restorative therapy; polymorphic; ds.
XX
OS Homo sapiens.
XX
XX WO200140521-A2.
PN
XX
PD 07-JUN-2001.
XX
XX
PF 30-NOV-2000; 2000MO-US32758.
XX
XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
PI Shinkets RA, Leach M;
XX
XX WPI; 2001-356160/37.
DR
XX

XX The invention relates to a method for controlling the activity of an
CC immunologically functional molecule (e.g., an antibody) where the
CC control is effected by the presence or absence of a sugar bound to an
CC N-acetylglucosamine residue at the reducing end of the sugar chain on
CC the immunologically functional molecule. The invention also relates to
CC methods for the diagnosis, prevention or treatment of diseases which
CC involve the modified immunologically functional molecule, and agents
CC which stimulate the activity of an immunologically functional molecule.
CC The methods of the invention are used for the diagnosis, treatment and
CC prevention of a broad range of diseases including cancer, circulatory
CC disease, viral or bacterial infection, allergy, autoimmune disease and
CC inflammation. The present sequence represents a Chinese hamster/rat
CC beta-actin PCR primer used in an exemplification of the invention.
XX
SQ Sequence 40 BP; 10 A; 5 C; 16 G; 9 T; 0 other;

Query Match 45.0%; Score 16.2; DB 21; Length 40;
Best Local Similarity 85.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 aactgcagagtgcttgg 26
|||||
Db 5 aactgcagagtgcttgg 25

RESULT 11
AAZ37381/C
ID AAZ37381 standard; DNA; 20 BP.
XX

AC AAZ37381;

DT 04-FEB-2000 (first entry)

DE PCR primer for human Bcl-2 gene.

XX Bcl-2; human; PCR primer; adenoviral vector; anti-apoptotic gene;
KW Ischaemia; reperfusion injury; liver; organ preservation;
KM endothelial cell cryoprotection; ss.
XX

OS Synthetic.

OS Homo sapiens.

PN WO955382-A1.

PD 04-NOV-1999.

PF 29-APR-1999; 99WO-US09412.

PR 29-APR-1999; 98US-0083434.

PA (UABR-) UAB RES FOUND.

PI Bilbao G, Curriel DT, Contreras JL;

DR WPI: 2000-023269/02.

PT Adenoviral vector encoding anti-apoptotic Bcl-2 gene useful for
PT cytoprotection and in gene therapy -
XX

PS Example 9; Page 26; 89pp; English.

CC This sequence represents a PCR primer for the human Bcl-2 gene. The
CC invention relates to an adenoviral vector encoding an anti-apoptotic
CC Bcl-2 gene. The adenoviral vector may be used to reduce
CC ischaemia/reperfusion injury in the liver, improve organ preservation,
CC cytoprotect endothelial cells or pancreatic islet cells during cold
CC preservation, or enhance or prolong the expression of a transgene. The
CC co-expression of Bcl-2 with a transgene mediated a significant reduction
CC in apoptosis and necrosis following adenovirus mediated gene transfer,
CC and an enhancement of transgene expression (up to 2 log).

SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 other;

Query Match 44.4%; Score 16; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 ttgtgactgtgacg 36
|||||
Db 20 TTGTGTAAGTGTACG 5

RESULT 12
AAT14539
ID AAT14539 standard; DNA; 34 BP.
XX

AC AAT14539;

DT 10-SEP-1996 (first entry)

DE Fc receptor PCR primer LR3.

XX Fc receptor; Fc gamma RI; Fc epsilon RI; IgE; autoimmune disease;
KW therapy; polymerase chain reaction; PCR; primer; ss.
XX

OS Synthetic.

PN WO9608512-A1.

PD 21-MAR-1996.

PF 15-SEP-1995; 95WO-AU00606.

PR 31-OCT-1994; 94US-0332562.

PR 16-SEP-1994; 94AU-0008232.

PA (AUST-) AUSTIN RES INST CANCER & ANTI INFLAMMATORY SYNDICATE NO.1.

PI Baker RI, Hogarth PM, Hulett MD, McKenzie IFC, Powell MS;

DR WPI: 1996-179903/18.

XX New mutant Fc receptor polypeptide(s) - have amino acid changes to
PT improve characteristics, e.g. half life, used partic in diagnosis or
PT treatment of auto-immune diseases
XX

PS Example 5; Page 48; 104pp; English.

CC Antisense PCR primer LR3 (AAT14539) was used with sense primer NR1
CC (AAT14531) and with primer pair LR4 + EG5 (AAT14540 + AAT14532) to
CC construct cDNA coding for chimeric receptor CC', comprising a
CC receptor with domain 1 from Fc gamma RI, domain 2 from Fc
CC epsilon RI, a transmembrane region from Fc gamma RI and the CC'
CC loop from Fc epsilon RI. The chimeric receptor was expressed by
CC transfected COS monolayers. Rosetting assays showed that the
CC transfected cells rosetted less well than either transfectants
CC (see also AAT14537-38 and AAT14541-42).
XX

SQ Sequence 34 BP; 6 A; 11 C; 8 G; 9 T; 0 other;

Query Match 43.9%; Score 15.8; DB 17; Length 34;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 11 cagagtgcttgggaac 29
|||||
Db 13 cagagtgcttgggaac 31

RESULT 13
AAN90551
ID AAN90551 standard; cDNA; 36 BP.

```

XX AC AAN90551;
XX DT 13-DEC-1989 (first entry)
XX DE Tissue plasminogen activator mutant KC2 (T255P: W256F: N451Q).
XX KW Tissue plasminogen activator; mutant; fibrinolysis; KC2 (T255P: W259R:
XX N451Q)
XX OS Homo sapiens.
XX FH Key
XX FT old_sequence
XX FT /*tag= a
XX FT replace(21..22, "")
XX FT old_sequence
XX FT /*tag= b
XX PN W08907146-A.
XX PD 10-AUG-1989.
XX PF 03-FEB-1989; 89WO-US00465.
XX PR 05-FEB-1988; 88US-0152692.
XX PA (INTE-) INTEGRATED GENETICS INC.
XX PI Markland W, Livingston DJ;
XX DR WPI; 1989-249015/34.
XX DR P-PSDB; AAP91270.
XX PT Rearranged tissue plasminogen activators - prepd. by altering the DNA
XX PT sequence to introduce Avrii, NheI, SpeI or XbaI cleavage sites.
XX PS Claim 11; page 58; 77pp; English.
XX CC The mutant is adapted for predictable rearrangement or deletion by
XX CC altering 2 or more pre-existing restriction sites to create sites
XX CC susceptible to cleavage by 1 or more of Avrii, NheI, SpeI and XbaI.
XX CC The sites are found at the C-terminus of the Kringle 2 domain.
XX CC See also AAP1270.
XX SQ Sequence 36 BP; 9 A; 8 C; 12 G; 7 T; 0 other;

Query Match 43.9%; Score 15.8; DB 10; Length 36;
Best Local Similarity 74.1%; Pred. No. 3.3e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 6 aactgcagatgccttctgtgaactgt 32
    ||| ||||| ||||| ||| |||||
DB 7 aacgcagcgcgcctcaggaggaactgt 33

RESULT 14
AAC90375
ID AAC90375 standard; DNA: 43 BP.
XX AC AAC90375;
XX DT 19-MAR-2001 (first entry)
XX DE pc4Fc:METH1 PCR primer #2.
XX MEH: metalloprotease; thrombospondin; angiogenesis inhibition;
XX cancer therapy; benign tumour; ocular angiogenic disease; PCR primer;
XX rheumatoid arthritis; psoriasis; wound healing; endometriosis;
XX vasculogenesis; granululation; hypertrophic scar; nonunion fracture;
XX scleroderma; trachoma; vascular adhesion; myocardial angiogenesis;
XX coronary collateral; cerebral collateral; arteriovenous malformation;
XX ischaemic limb angiogenesis; Osler-Webber syndrome; wound granululation;

```

```

KW plaque neovascularisation; telangiectasia; haemophilic joint; EST;
KW angiofibroma; fibromuscular dysplasia; expressed sequence tag;
KW Crohn's disease; atherosclerosis; birth control; ss.
XX OS Homo sapiens.
XX PN W0200071577-A1.
XX PD 30-NOV-2000.
XX PF 25-MAY-2000; 2000WO-US14462.
XX PR 25-MAY-1999; 99US-0318208.
XX PR 20-JUL-1999; 99US-0144882.
XX PR 10-AUG-1999; 99US-0147823.
XX PR 13-AUG-1999; 99US-0373658.
XX PR 22-DEC-1999; 99US-0171503.
XX PR 22-FEB-2000; 2000US-0183792.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (SMK) SMITHKLINE BEECHAM CORP.
XX PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX PA (IRUE/) IRUELA-ARISPE L.
XX PA (HASY/) HASTINGS G A.
XX PA (RUBE/) RUBEN S M.
XX PA (JONA/) JONAK Z L.
XX PA (TRUI/) TRULLI S H.
XX PA (FORN/) FORNWALD J A.
XX PA (TERR/) TERRETT J A.
XX PI IrueLA-Arispe L, Hastings GA, Ruben SM, Jonak ZL, Trulli SH;
XX PI Fornwald JA, Terrett JA.
XX DR WPI; 2001-025136/03.
XX PT METH1 and METH2 polynucleotides and encoded polypeptides, used to
XX PT inhibit angiogenesis in the treatment of disorders such as cancer,
XX PT rheumatoid arthritis and psoriasis -
XX PS Example 52; Page 479; 768pp; English.
XX CC The present invention relates to human METH1 and METH2, (ME for
XX CC metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).
XX CC The present sequence is a PCR primer used in the present invention. METH
XX CC can be used for inhibiting angiogenesis in an individual, and for
XX CC treating cancer, benign tumours, an ocular angiogenic disease,
XX CC rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis,
XX CC vasculogenesis, granululations, hypertrophic scars, nonunion fractures,
XX CC scleroderma, trachoma, vascular adhesions, myocardial angiogenesis,
XX CC coronary collaterals, cerebral collaterals, arteriovenous malformations,
XX CC ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
XX CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
XX CC fibromuscular dysplasia, wound granululation, Crohn's disease or
XX CC atherosclerosis. METH can also be used in birth control. METH can also
XX CC be used in diagnostic methods for the prognosis of cancer.
XX SQ Sequence 43 BP; 11 A; 10 C; 9 G; 13 T; 0 other;

Query Match 43.9%; Score 15.8; DB 22; Length 43;
Best Local Similarity 74.1%; Pred. No. 3.4e+03;
Matches 20; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 6 aactgcagatgccttctgtgaactgt 32
    ||||| ||||| ||||| ||| |||||
DB 12 aactgcattcttcattgtgcaaaagt 38

RESULT 15
AAB24317/c
ID AAB24317 standard; DNA: 31 BP.
XX AC AAB24317;

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:43 ; Search time 334.55 Seconds
(without alignments)
26.432 Million cell updates/sec

Title: US-09-709-170A-6

Perfect score: 36
Sequence: 1 cccccacgcagatgccttctgtgaactgtacgg 36

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*

1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/lna/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/PCITUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	1	US-08-217-082A-6 Sequence 6, Appli
2	36	100.0	36	2	US-08-465-485A-6 Sequence 6, Appli
3	36	100.0	36	3	US-09-080-285-6 Sequence 6, Appli
4	24	66.7	34	1	US-07-936-421-16 Sequence 16, Appli
5	20	55.6	20	1	US-08-217-082A-5 Sequence 5, Appli
6	20	55.6	20	2	US-08-465-485A-5 Sequence 5, Appli
7	20	55.6	20	3	US-09-080-285-5 Sequence 5, Appli
8	15.4	42.8	30	4	US-09-053-871A-4 Sequence 4, Appli
9	15.4	42.8	31	4	US-09-053-871A-5 Sequence 5, Appli
10	15.4	42.8	32	4	US-09-053-871A-6 Sequence 6, Appli
11	15.2	42.2	20	3	US-09-288-461-83 Sequence 83, Appli
12	15.2	42.2	20	4	US-09-167-921-35 Sequence 35, Appli
13	15.2	42.2	20	4	US-09-277-020-46 Sequence 46, Appli
14	15.2	42.2	20	4	US-09-323-743-35 Sequence 35, Appli
15	15.2	42.2	27	3	US-08-513-974B-87 Sequence 87, Appli
16	15.2	42.2	30	4	US-09-053-871A-20 Sequence 20, Appli
17	15.2	42.2	40	2	US-08-425-684-19 Sequence 19, Appli
18	15.2	42.2	40	2	US-08-675-502-19 Sequence 19, Appli
19	15.2	42.2	60	2	US-08-663-566A-47 Sequence 47, Appli
20	15.2	42.2	60	2	US-08-023-610-47 Sequence 47, Appli
21	15.2	42.2	60	2	US-08-288-065A-47 Sequence 47, Appli
22	15.2	42.2	60	2	US-08-362-240A-47 Sequence 47, Appli
23	15.2	42.2	60	5	PCT-US95-10245-47 Sequence 47, Appli
24	15.2	42.2	63	3	US-08-969-320-1 Sequence 1, Appli
25	15.2	42.2	49	4	US-08-718-388-10 Sequence 10, Appli
26	15.2	42.2	54	1	US-08-484-686B-25 Sequence 25, Appli
27	15.2	42.2	54	4	US-08-463-160B-25 Sequence 25, Appli

28	15	41.7	54	5	PCT-US91-02568-26	Sequence 26, Appli
29	14.8	41.1	38	1	US-08-358-810A-1	Sequence 1, Appli
30	14.8	41.1	38	1	US-08-484-712A-1	Sequence 1, Appli
31	14.8	41.1	38	1	US-08-359-295C-3	Sequence 3, Appli
32	14.8	41.1	38	1	US-08-659-453B-5	Sequence 5, Appli
33	14.8	41.1	38	2	US-08-485-105A-3	Sequence 3, Appli
34	14.8	41.1	38	3	US-09-089-853A-5	Sequence 5, Appli
35	14.8	41.1	38	3	US-09-183-650-3	Sequence 3, Appli
36	14.8	41.1	38	3	US-09-196-543D-5	Sequence 5, Appli
37	14.8	41.1	38	4	US-09-131-009A-5	Sequence 5, Appli
38	14.8	41.1	38	4	US-09-092-226A-5	Sequence 5, Appli
39	14.8	41.1	38	4	US-09-269-911A-3	Sequence 3, Appli
40	14.8	41.1	38	4	US-09-130-862A-5	Sequence 5, Appli
41	14.8	41.1	38	4	US-09-090-809A-5	Sequence 5, Appli
42	14.8	41.1	38	4	US-09-053-116A-5	Sequence 5, Appli
43	14.8	41.1	45	1	US-08-291-299-3	Sequence 3, Appli
44	14.8	41.1	45	5	PCT-US95-10579-3	Sequence 3, Appli
45	14.6	40.6	71	4	US-09-363-939A-38	Sequence 38, Appli

ALIGNMENTS

RESULT 1
US-08-217-082A-6
Sequence 6, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUBADT,
ADDRESS: P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-6

Query Match 100.0%; Score 36; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cccccactgcagatgccttctgtggaactgtacg 36
|||||
Db 1 cccccactgcagatgccttctgtggaactgtacg 36

RESULT 2

US-08-465-485A-6
; Sequence 6, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2070
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-08-465-485A-6

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cccccactgcagatgccttctgtggaactgtacg 36
|||||
Db 1 cccccactgcagatgccttctgtggaactgtacg 36

RESULT 3
US-09-080-285-6
; Sequence 6, Application US/09080285

; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C.
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: NO
; US-09-080-285-6

Query Match 100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cccccactgcagatgccttctgtggaactgtacg 36
|||||
Db 1 cccccactgcagatgccttctgtggaactgtacg 36

RESULT 4
US-07-936-421-16
; Sequence 16, Application US/07936421
; Patent No. 5750390
; GENERAL INFORMATION:
; APPLICANT: James D. Thompson
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: TREATMENT OF DISEASES CAUSED
; TITLE OF INVENTION: BY EXPRESSION OF THE BCL-2
; NUMBER OF SEQUENCES: 22

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 611 West Sixth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90017
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;; SOFTWARE: WordPerfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/936,421
;; FILING DATE: 19920826
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION DATA: including application
;; PRIOR APPLICATION DATA: described below:
;; APPLICATION NUMBER: none
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER: 197/243
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 34
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-07-936-421-16

Query Match 66.7%; Score 24; DB 1; Length 34;
Best Local Similarity 70.8%; Pred. No. 0.22;
Matches 17; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 13 ggaatccttgggaactgtacg 36
|||||:|:|:|:|:|:|:|:|:|
Db 1 GGAUGCCUUGUGGACUGUACGG 24

RESULT 5
US-08-217-082A-5/C
; Sequence 5, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,082A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/840,716
;; FILING DATE: 21-FEB-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/288,692
;; FILING DATE: 22-DEC-1988
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fortney, Andrew D.
;; REGISTRATION NUMBER: 34,600
;; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (408) 436-2070
;; TELEFAX: (408) 436-2075
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: Synthetic DNA
;; ANTI-SENSE: YES
;; US-08-217-082A-5

Query Match 55.6%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 caactgcaggatgccttgt 24
|||||:|:|:|:|:|:|:|:|:|
Db 20 CAACGCGAGAGATGCTTGTG 1

RESULT 6
US-08-465-485A-5/C
; Sequence 5, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-5

Query Match 55.6%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 caactgcagatgccttctgt 24
|||||
DB 20 CAACTGCAGATGCCTTTGT 1

RESULT 7
US-09-080-285-5/C
Sequence 5, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
City: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES
US-09-080-285-5

Query Match 55.6%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 caactgcagatgccttctgt 24
|||||
DB 20 CAACTGCAGATGCCTTTGT 1

RESULT 8
US-09-053-871A-4/C
Sequence 4, Application US/09053871A
Patent No. 6315995
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
APPLICANT: Stern, David
APPLICANT: Rose, Eric
APPLICANT: Solomon, Robert A.
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
FILE REFERENCE: 51917-B
CURRENT APPLICATION NUMBER: US/09/053,871A
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotides for producing factor Ixm1.
OTHER INFORMATION: NNN-the complement to a DNA codon for any one of
OTHER INFORMATION: the standard amino acids other than serine.
US-09-053-871A-4

Query Match 42.8%; Score 15.4; DB 4; Length 30;
Best Local Similarity 67.9%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 7 actgcagatgccttctgtggaactgtac 34
|||||
DB 28 ACCCCAGGGGNNNTAGAGGAACTGTAC 1

RESULT 9
US-09-053-871A-5/C
Sequence 5, Application US/09053871A
Patent No. 6315995
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
APPLICANT: Stern, David
APPLICANT: Rose, Eric
APPLICANT: Solomon, Robert A.
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
FILE REFERENCE: 51917-B
CURRENT APPLICATION NUMBER: US/09/053,871A
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotides for producing Factor IXm1.
OTHER INFORMATION: NNN-the complement to a DNA codon for any one of
OTHER INFORMATION: the standard amino acids other than serine.
US-09-053-871A-5

Query Match 42.8%; Score 15.4; DB 4; Length 31;
Best Local Similarity 67.9%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 7 actgacgagatgccttctgtgactgtac 34
|| ||||| | | |||||
Db 28 ACCCAGGCGGNNMTAGAGAACTGTAC 1

RESULT 10
US-09-053-871A-6/c
Sequence 6, Application US/09053871A
Patent No. 6315995
GENERAL INFORMATION:
APPLICANT: Pinsky, David J.
APPLICANT: Stern, David
APPLICANT: Rose, Eric
APPLICANT: Solomon, Robert A.
APPLICANT: Schmidt, Ann Marie
TITLE OF INVENTION: METHODS FOR TREATING AN ISCHEMIC DISORDER AND IMPROVING
TITLE OF INVENTION: STROKE OUTCOME
FILE REFERENCE: 51917-B
CURRENT APPLICATION NUMBER: US/09/053, 871A
CURRENT FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 6
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotides for producing Factor IXm1.
OTHER INFORMATION: NNN-the complement to a DNA codon for any one of
OTHER INFORMATION: the standard amino acids other than serine.
US-09-053-871A-6

Query Match 42.8%; Score 15.4; DB 4; Length 32;
Best Local Similarity 67.9%; Pred. No. 6.7e+02;
Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 7 actgacgagatgccttctgtgactgtac 34
|| ||||| | | |||||
Db 28 ACCCAGGCGGNNMTAGAGAACTGTAC 1

RESULT 11
US-09-288-461-83/c
Sequence 83, Application US/09288461
Patent No. 6139694
GENERAL INFORMATION:
APPLICANT: Karas, James G.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
FILE REFERENCE: ISPH-0338
CURRENT APPLICATION NUMBER: US/09/288, 461
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 83
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence

US-09-288-461-83

Query Match 42.2%; Score 15.2; DB 3; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 gcagatgccttctgtgaaac 29
|| ||||| | | |||||
Db 20 GCAGATGCTCTCACTGGAAC 1

RESULT 12
US-09-167-921-35/c
Sequence 35, Application US/09167921A
Patent No. 6172216
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Dean, Nicholas M.
APPLICANT: Monia, Brett P.
APPLICANT: Nickoloff, Brian J.
APPLICANT: Zhang, QingQing
TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
FILE REFERENCE: ISPH-0324
CURRENT APPLICATION NUMBER: US/09/167, 921A
CURRENT FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 35
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense sequence
US-09-167-921-35

Query Match 42.2%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 14 gatccttctgtgactgtac 33
|| | ||||| |||||
Db 20 GATCTTTTGTGCACTCTA 1

RESULT 13
US-09-277-020-46/c
Sequence 46, Application US/09277020
Patent No. 6210892
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: Alteration of Cellular Behavior by Antisense Modulation
FILE REFERENCE: ISPH-0339
CURRENT APPLICATION NUMBER: US/09/277, 020
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 09/167, 921
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 46
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-277-020-46

Query Match 42.2%; Score 15.2; DB 4; Length 20;
Best Local Similarity 85.0%; Pred. No. 7.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 14 gatgccttctggaactgta 33
20 GATACCTTTGTGGAACCTCTA 1

RESULT 14
US-09-323-743-35/C

Sequence 35, Application US/09323743

Patent No. 6214986

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Dean, Nicholas M.

APPLICANT: Monia, Brett P.

APPLICANT: Nickoloff, Brian J.

APPLICANT: Zhang, Qinqiong

TITLE OF INVENTION: Antisense Modulation of bcl-x Expression

FILE REFERENCE: ISPH-0368

CURRENT APPLICATION NUMBER: US/09/323,743

CURRENT FILING DATE: 1999-06-01

EARLIER APPLICATION NUMBER: 09/277,020

EARLIER FILING DATE: 1998-03-26

EARLIER APPLICATION NUMBER: 09/167,921

EARLIER FILING DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 66

SOFTWARE: Patentin Ver. 2.0

SEO ID NO 35

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-323-743-35

Query Match 42.2%; Score 15.2; DB 4; Length 20;

Best Local Similarity 85.0%; Pred. No. 7.3e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 14 gatgccttctggaactgta 33

20 GATACCTTTGTGGAACCTCTA 1

RESULT 15

US-08-513-974B-87

Sequence 87, Application US/08513974B

Patent No. 6114139

GENERAL INFORMATION:

APPLICANT: Hinuma, Shuji

APPLICANT: Hosoya, Masaki

APPLICANT: Fujii, Ryo

APPLICANT: Ohtaki, Tetsuya

APPLICANT: Fukusumi, Shoji

APPLICANT: Ohgi, Kazuhito

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

TITLE OF INVENTION: PRODUCTION, AND USE THEREOF

NUMBER OF SEQUENCES: 380

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

STREET: 130 Water Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/513,974B

FILING DATE: 14-SEP-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP95/01599

FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-093989

FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-057186

FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-326611

FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-270017

FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-236357

FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-236356

FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189274

FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189273

FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-189272

FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Resnick, David S.

REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 45753

TELEPHONE: 617-523-3400

TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-513-974B-87

Query Match 42.2%; Score 15.2; DB 3; Length 27;

Best Local Similarity 85.0%; Pred. No. 7.8e+02;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 5 caactgagatgacttctgt 24

6 CATCTGCTGATGCTTCTTCT 25

Search completed: June 28, 2002, 22:16:44

Job time: 8270 sec

Mon Jul 1 08:40:58 2002

us-09-709-170a-6.szlm75.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:01 ; Search time 3762.88 Seconds

(without alignments)
111.226 Million cell updates/sec

Title: US-09-709-170A-7

Perfect score: 20

Sequence: 1 ggggaagatgagcagcagctg 20

Scoring table: IDENTITY_NUC

Gap 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
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29: em.vl:*
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31: em.htg.inv:*
32: em.htg.other:*
33: em.htgo.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
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c	1	20	100.0	20	6	AR052603	AR052603 Sequence
c	2	20	100.0	20	6	AR052609	AR052609 Sequence
c	3	20	100.0	20	6	AR176022	AR176022 Sequence
c	4	20	100.0	20	6	AR176023	AR176023 Sequence
c	5	20	100.0	20	6	AR211659	AR211659 Sequence
c	6	20	100.0	20	6	AX211670	AX211670 Sequence
c	7	20	100.0	20	6	AX277461	AX277461 Sequence
c	8	20	100.0	20	6	196082	196082 Sequence 1
c	9	20	100.0	20	6	196088	196088 Sequence 7
c	10	20	100.0	22	6	A76123	A76123 Sequence 3
c	11	20	100.0	22	6	A76124	A76124 Sequence 4
c	12	20	100.0	35	6	AR052604	AR052604 Sequence
c	13	20	100.0	35	6	196083	196083 Sequence 2
c	14	18	95.0	20	6	AX045387	AX045387 Sequence
c	15	19	90.0	18	6	BD008994	BD008994 Inhibitor
c	16	17	85.0	17	6	196092	196092 Sequence 11
c	17	16	80.0	17	6	196091	196091 Sequence 10
c	18	15.8	79.0	51	6	AX165740	AX165740 Sequence
c	19	15.4	77.0	29	5	CHRC2A101	K02260 Chicken alp
c	20	15	75.0	15	6	AX277468	AX277468 Sequence
c	21	15	75.0	15	6	AX277469	AX277469 Sequence
c	22	15	75.0	17	6	196093	196093 Sequence 12
c	23	14	70.0	19	6	AX083694	AX083694 Sequence
c	24	13.8	69.0	50	6	AX113707	AX113707 Sequence
c	25	13.8	69.0	60	6	AX113708	AX113708 Sequence
c	26	13.8	69.0	70	6	AX113709	AX113709 Sequence
c	27	13.6	68.0	27	6	AR004426	AR004426 Sequence
c	28	13.6	68.0	27	6	143661	143661 Sequence 13
c	29	13.6	68.0	27	6	186720	186720 Sequence 8
c	30	13.4	67.0	24	6	AX290202	AX290202 Sequence
c	31	13.2	66.0	47	6	AR153764	AR153764 Sequence
c	32	13.2	66.0	47	6	AR153766	AR153766 Sequence
c	33	13.2	66.0	51	6	AX157777	AX157777 Sequence
c	34	13.2	66.0	51	6	AX157778	AX157778 Sequence
c	35	13.2	66.0	51	6	AX157779	AX157779 Sequence
c	36	13	65.0	16	6	AX103898	AX103898 Sequence
c	37	13	65.0	16	6	AX355505	AX355505 Sequence
c	38	13	65.0	17	6	196090	196090 Sequence 9
c	39	13	65.0	18	6	AR052619	AR052619 Sequence
c	40	13	65.0	18	6	AR052624	AR052624 Sequence
c	41	13	65.0	18	6	AR116926	AR116926 Sequence
c	42	13	65.0	18	6	AR140496	AR140496 Sequence
c	43	13	65.0	18	6	AR146347	AR146347 Sequence
c	44	13	65.0	18	6	AR146392	AR146392 Sequence
c	45	13	65.0	18	6	AR154716	AR154716 Sequence

ALIGNMENTS

RESULT 1

AR052603/c AR052603 20 bp DNA

LOCUS AR052603 11near PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5831066.

ACCESSION AR052603

VERSION AR052603.1 GI:5975967

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 20)

AUTHORS Reed J.C.

TITLE Regulation of bcl-2 gene expression

JOURNAL Patent: US 5831066-A1 03-NOV-1998;

FEATURES

source Location/Qualifiers

BASE COUNT 2 a 10 c 4 g 4 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;

Best local similarity 100.0%; Pred. No. 50;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatggcgacgctg 20
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Db 20 GGGAAGATGGCGCAGCTG 1

RESULT 2
AR052609
LOCUS AR052609 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 7 from patent US 5831066.
ACCESSION AR052609
VERSION AR052609.1 GI:5975973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 7 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatggcgacgctg 20
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Db 1 GGGAAGATGGCGCAGCTG 20

RESULT 3
AR176022/c
LOCUS AR176022 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6310047.
ACCESSION AR176022
VERSION AR176022.1 GI:17917321
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 1 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatggcgacgctg 20
|||||
Db 20 GGGAAGATGGCGCAGCTG 1

RESULT 4
AR176023
LOCUS AR176023 20 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 2 from patent US 6310047.
ACCESSION AR176023

VERSION AR176023.1 GI:17917322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Farrell,N. and Kloster,M.
TITLE High affinity DNA binding compounds as adjuvants in antisense technology
JOURNAL Patent: US 6310047-A 2 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatggcgacgctg 20
|||||
Db 1 GGGAAGATGGCGCAGCTG 20

RESULT 5
AX211669
LOCUS AX211669 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 1 from Patent WO0159156.
ACCESSION AX211669
VERSION AX211669.1 GI:15523901
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatt,S.
TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 1 16-AUG-2001;
Yissum Research Development Co., the Hebrew University of Jerusalem (IL)

FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="..."

BASE COUNT 4 a 4 c 10 g 2 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatggcgacgctg 20
|||||
Db 1 GGGAAGATGGCGCAGCTG 20

RESULT 6
AX211670/c
LOCUS AX211670 20 bp DNA linear PAT 06-SEP-2001
DEFINITION Sequence 2 from Patent WO0159156.
ACCESSION AX211670
VERSION AX211670.1 GI:15523902
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Barenholz,Y., Hirsch-Lerner,D., Cohen,R., Dagan,A. and Gatt,S.

TITLE Detection of binding of charged species using ph- or potential-sensitive probes
JOURNAL Patent: WO 0159156-A 2 16-AUG-2001;
Yissam Research Development Co., the Hebrew University of Jerusalem (II)

FEATURES
source 1. .20
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="."

BASE COUNT 2 a 10 c 4 g 4 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggaagatgagcgacgctg 20
|||||

Db 20 GGGAAGATGGCGACGCTG 1

RESULT 7
AX277461/c 20 bp DNA linear PAT 29-OCT-2001
LOCUS Sequence 1 from Patent WO0160998.
DEFINITION AX277461
ACCESSION AX277461
VERSION AX277461.1 GI:16548979
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
TAXON 32630
/note="Synthetic Primer"

REFERENCE
AUTHORS Tarl, A.M., Lopez-Berestein, G. and Gutierrez-Puente, Y.
TITLE Small oligonucleotides with anti-tumor activity
JOURNAL Patent: WO 0160998-A 1 23-AUG-2001;
Board of Regents, The University of Texas System (US)
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic Primer"

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 GGGAAGATGGCGACGCTG 1

RESULT 8
196082/c 20 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 1 from patent US 5734033.
DEFINITION 196082
ACCESSION 196082
VERSION 196082.1 GI:3940552
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
TAXON 32630
/note="Synthetic Primer"

REFERENCE
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 1 31-MAR-1998;
Location/Qualifiers
1. .20
/organism="unknown"

BASE COUNT 2 a 10 c 4 g 4 t

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Best Local Similarity 100.0%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gggaagatgagcgacgctg 20
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Db 20 GGGAAGATGGCGACGCTG 1

RESULT 9
196088 20 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 7 from patent US 5734033.
DEFINITION 196088
ACCESSION 196088
VERSION 196088.1 GI:3940558
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
TAXON 32630
/note="Synthetic Primer"

REFERENCE
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 7 31-MAR-1998;
Location/Qualifiers
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BASE COUNT 4 a 10 c 4 g 10 g 2 t

ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGAAGATGGCGACGCTG 20

RESULT 10
A76123/c 22 bp DNA linear PAT 19-OCT-1999
LOCUS Sequence 3 from Patent WO9320200.
DEFINITION A76123
ACCESSION A76123
VERSION A76123.1 GI:6088259
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
TAXON 32630
/note="Synthetic Primer"

REFERENCE
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: NO 9320200-A 3 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERRARD IAN (GB)
Location/Qualifiers
1. .22
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/db_xref="taxon:32644"

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ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 22 GGGAAGATGGCGACGCTG 3

RESULT 11
A76124/c 22 bp DNA linear PAT 19-OCT-1999
LOCUS Sequence 4 from Patent WO9320200.
DEFINITION A76124
ACCESSION A76124
VERSION A76124.1 GI:6088260
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Evan, G.I.
TITLE MODIFIED CELLS AND METHOD OF TREATMENT
JOURNAL Patent: WO 9320200-A 4 14-OCT-1993;
IMP CANCER RES TECH (GB); EVAN GERARD IAN (GB)
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location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 2 a 12 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 50;
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Db 22 GGGAAGATGGCGCAGCTG 3

RESULT 12
AR052604 35 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 2 from patent US 5831066.
DEFINITION AR052604
ACCESSION AR052604
VERSION AR052604.1 GI:5975968
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 2 03-NOV-1998;
FEATURES location/Qualifiers
source 1..35
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BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 13
I96083 35 bp DNA linear PAT 01-DEC-1998
LOCUS Sequence 2 from patent US 5734033.
DEFINITION I96083
ACCESSION I96083
VERSION I96083.1 GI:3940553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 35)
AUTHORS Reed, J.
TITLE Antisense oligonucleotides inhibiting human bcl-2 gene expression
JOURNAL Patent: US 5734033-A 2 31-MAR-1998;
FEATURES location/Qualifiers
source 1..35
/organism="unknown"
BASE COUNT 6 a 8 c 13 g 8 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 35;
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Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 14
AX045387/c 20 bp DNA linear PAT 24-NOV-2000
LOCUS Sequence 7 from Patent WO0066724.
DEFINITION AX045387
ACCESSION AX045387
VERSION AX045387.1 GI:11343871
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zangmeister-Wittke, U., Luedke, G. and Huesken, D.
TITLE bcl-2 mrna
JOURNAL Patent: WO 0066724-A 7 09-NOV-2000;
FEATURES location/Qualifiers
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/db_xref="taxon:32630"
/note="Antisense"
BASE COUNT 2 a 10 c 4 g 4 t
ORIGIN

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 GGGAAGATGGCGCAGCTG 2

RESULT 15
BD008994/c 18 bp DNA linear PAT 31-JAN-2002
LOCUS Inhibition of bcl-2 protein expression by liposomal antisense
DEFINITION BD008994
ACCESSION BD008994
VERSION BD008994.1 GI:18637367
KEYWORDS JP 2001502172-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Tormo, M., Tara, A.M., Berenstein, G.L. and McDonnell, T.J.
TITLE Inhibition of bcl-2 protein expression by liposomal antisense
JOURNAL Patent: JP 2001502172-A 1 20-FEB-2001.
COMMENT BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM
OS Unidentified

PN JP 2001502172-A/1
 PD 20-FEB-2001
 PE 03-OCT-1997 JP 1998516985
 PR 04-OCT-1996 US 08/726211
 PI MAR TORMO,ANA M TARA,GABRIEL LOPEZ BERESTEIN, PI TIMOTHY J
 MCDONNELL

PC A6IK9/127,A6IK31/70,C07H21/04,C12N15/00
 CC Strandedness: Single;
 CC Topology: Linear;
 FH key Location/Qualifiers
 FT source 1.18
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 /organism="unidentified"
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FEATURES
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 BASE COUNT 2 a 8 c 4 g 4 t
 ORIGIN

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 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 gaagagatggcgacgctg 20
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 Db 18 GAAGGATGGCGACGCTG 1

Search completed: June 28, 2002, 22:11:03
 Job time: 8354 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:44 ; Search time 334.55 seconds
(without alignments)
14.664 Million cell updates/sec

Title: US-09-709-170A-7

Perfect score: 20

Sequence: 1 gggagagatgagcagcagctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
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c 2	20	100.0	20	1	US-08-217-082A-7	Sequence 7, Appl
c 3	20	100.0	20	2	US-08-465-485A-1	Sequence 1, Appl
c 4	20	100.0	20	2	US-08-465-485A-7	Sequence 7, Appl
c 5	20	100.0	20	3	US-09-080-285-1	Sequence 1, Appl
c 6	20	100.0	20	3	US-09-080-285-7	Sequence 7, Appl
c 7	20	100.0	20	4	US-09-379-718-1	Sequence 1, Appl
c 8	20	100.0	20	4	US-09-379-718-2	Sequence 2, Appl
c 9	20	100.0	35	1	US-08-217-082A-2	Sequence 2, Appl
c 10	20	100.0	35	2	US-08-465-485A-2	Sequence 2, Appl
c 11	20	100.0	35	3	US-09-080-285-2	Sequence 2, Appl
c 12	17	85.0	17	1	US-08-217-082A-11	Sequence 11, Appl
c 13	16	80.0	17	1	US-08-217-082A-10	Sequence 10, Appl
c 14	15	75.0	17	1	US-08-217-082A-12	Sequence 12, Appl
c 15	13	68.0	27	1	US-08-410-804-13	Sequence 13, Appl
c 16	13	68.0	27	1	US-08-607-269-8	Sequence 8, Appl
c 17	13	68.0	27	1	US-08-259-514-13	Sequence 13, Appl
c 18	13	68.0	27	2	US-08-856-311-13	Sequence 13, Appl
c 19	13	68.0	27	5	PCT-US95-04600-8	Sequence 8, Appl
c 20	13	66.0	47	4	US-08-869-380-5	Sequence 5, Appl
c 21	13	66.0	47	4	US-08-869-380-7	Sequence 7, Appl
c 22	13	66.0	47	5	PCT-US95-13552-16	Sequence 16, Appl
c 23	13	66.0	47	5	PCT-US95-13552-18	Sequence 18, Appl
c 24	13	65.0	17	1	US-08-217-082A-9	Sequence 9, Appl
c 25	13	65.0	18	1	US-08-217-082A-17	Sequence 17, Appl
c 26	13	65.0	18	2	US-08-465-485A-17	Sequence 17, Appl
c 27	13	65.0	18	2	US-08-465-485A-24	Sequence 24, Appl

c 28	13	65.0	18	3	US-09-080-285-17	Sequence 17, Appl
c 29	13	65.0	18	3	US-09-080-285-24	Sequence 24, Appl
c 30	13	65.0	18	3	US-09-249-730-218	Sequence 218, Appl
c 31	13	65.0	18	3	US-09-118-220-1	Sequence 1, Appl
c 32	13	65.0	18	4	US-08-738-652-55	Sequence 55, Appl
c 33	13	65.0	18	4	US-09-030-701-27	Sequence 27, Appl
c 34	13	65.0	18	4	US-09-286-098-59	Sequence 59, Appl
c 35	13	65.0	18	4	US-09-286-098-104	Sequence 104, Appl
c 36	13	65.0	18	4	US-08-960-774-45	Sequence 45, Appl
c 37	13	65.0	18	4	US-09-078-934-14	Sequence 14, Appl
c 38	13	65.0	19	6	5276019-8	Patent No. 5276019
c 39	13	65.0	20	4	US-09-082-649B-60	Sequence 60, Appl
c 40	12.8	64.0	20	3	US-09-418-640-84	Sequence 84, Appl
c 41	12.6	63.0	32	4	US-09-272-496-5	Sequence 5, Appl
c 42	12.4	62.0	45	4	US-08-358-627F-1	Sequence 1, Appl
c 43	12.2	61.0	21	4	US-09-485-636-25	Sequence 25, Appl
c 44	12.2	61.0	30	5	PCT-US94-10257A-37	Sequence 37, Appl
c 45	12.2	61.0	33	3	US-08-816-346-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1

US-08-217-082A-1/C
; Sequence 1, Application US/08217082A

; Patent No. 5734033

; GENERAL INFORMATION:

; APPLICANT: Reed, John

; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,

; ADDRESS: P.C.

; STREET: 224 Airport Parkway

; CITY: San Jose

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 95110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/217,082A

; FILING DATE: 24-MAR-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/840,716

; FILING DATE: 21-FEB-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/288,692

; FILING DATE: 22-DEC-1988

; ATTORNEY/AGENT INFORMATION:

; NAME: Fortney, Andrew D.

; REGISTRATION NUMBER: 34,600

; REFERENCE/DOCKET NUMBER: 3335-067-55 FWC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (408) 436-2070

; TELEFAX: (408) 436-2075

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: Synthetic DNA

; ANTI-SENSE: YES

; US-08-217-082A-1

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 20 GGGAGAGATGGCGCACGCTG 1

RESULT 2
US-08-217-082A-7
; Sequence 7, Application US/08217082A
; Patent No. 5734033
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
; TITLE OF INVENTION: GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 224 Airport Parkway
; CITY: San Jose
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 95110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FMC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: NO
US-08-217-082A-7

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGAGAGATGGCGCACGCTG 20

RESULT 3
US-08-465-485A-1/C
; Sequence 1, Application US/08465485A

; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-1

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gggaaagatgagcgacgctg 20
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Db 20 GGGAGAGATGGCGCACGCTG 1

RESULT 4
US-08-465-485A-7
; Sequence 7, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-465-485A-7

Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
DB 1 ggggaagatggcgacgctg 20

RESULT 5
US-09-080-285-1/c
Sequence 1, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggggaagatggcgacgctg 20
DB 20 ggggaagatggcgacgctg 1

RESULT 6
US-09-080-285-7
Sequence 7, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-09-080-285-7

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggaagagatgagcagcctg 20
DB 1 GGAAGAGATGGCGACGCTG 20

RESULT 7
US-09-379-718-1/c
Sequence 1, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
APPLICANT: Kloster, Miriam
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
FILE REFERENCE: Antisense Technology
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-379-718-1

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggaagagatgagcagcctg 20
DB 20 GGAAGAGATGGCGACGCTG 1

RESULT 8
US-09-379-718-2
Sequence 2, Application US/09379718
Patent No. 6310047
GENERAL INFORMATION:
APPLICANT: Farrell, Nicholas
APPLICANT: Kloster, Miriam
TITLE OF INVENTION: High Affinity DNA Binding Compounds as Adjuvants in
FILE REFERENCE: Antisense Technology
CURRENT APPLICATION NUMBER: US/09/379,718
CURRENT FILING DATE: 1999-08-24

NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-379-718-2

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggaagagatgagcagcctg 20
DB 1 ggaagagatgagcagcctg 20

RESULT 9
US-08-217-082A-2
Sequence 2, Application US/08217082A
Patent No. 573403
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESS: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: NO
US-08-217-082A-2

Query Match 100.0%; Score 20; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 20: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
|||||
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 10

US-08-465-485A-2
; Sequence 2, Application US/08465485A
; Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,485A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

US-08-465-485A-2

Query Match 100.0%; Score 20; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
|||||
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 11

US-09-080-285-2

; Sequence 2, Application US/09080285

; Patent No. 6040181

; GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/465,485

FILING DATE: 05-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: NO

US-09-080-285-2

Query Match 100.0%; Score 20; DB 3; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgagcagctg 20
|||||
Db 11 GGGAAGATGGCGCAGCTG 30

RESULT 12

US-08-217-082A-11/C

; Sequence 11, Application US/08217082A

; Patent No. 5734033

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE

GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 224 Airport Parkway

CITY: San Jose

STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-11

Query Match 85.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 ggaagatggcgacgc 18
|||||
DB 17 ggaagatggcgacgc 1

RESULT 13
US-08-217-082A-10/c
Sequence 10, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-10

Query Match 80.0%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 agaatggcgacgcctg 20
|||||
DB 17 AGAATGGCGCACCGCTG 2

RESULT 14
US-08-217-082A-12/c
Sequence 12, Application US/08217082A
Patent No. 5734033
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR INHIBITING THE
GROWTH OF CELLS EXPRESSING THE HUMAN BCL-2 GENE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 224 Airport Parkway
CITY: San Jose
STATE: California
COUNTRY: U.S.A.
ZIP: 95110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,082A
FILING DATE: 24-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-067-55 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
US-08-217-082A-12

Query Match

Best Local Similarity 75.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gggaagatgcgcga 15
15 GGAAGATGCGCGCA 1

RESULT 15

US-08-410-804-13
Sequence 13, Application US/08410804
Patent No. 5632994

GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Sato, Takaki
TITLE OF INVENTION: FAS ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cathryn Campbell
STREET: 4370 La Jolla Village Drive, Ste 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,804
FILING DATE: 27-MAR-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/259,514
FILING DATE: 14-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1389
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-410-804-13

Query Match

Best Local Similarity 68.0%; Score 13.6; DB 1; Length 27;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 gggaagatgcgcgcgctg 20
1 GGAATGATGCGCGCGCTG 20

Mon Jul 1 08:40:59 2002

us-09-709-170a-7.szlm75.rni

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:03 ; Search time 3762.88 Seconds
(Without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170a-8
Perfect score: 17
Sequence: 1 cgcgcgcgcacctctg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
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2: gb_htg:*
3: gb_in:*
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21: em_or:*
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27: em_sts:*
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29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgc_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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RESULT	1	17	100.0	17	6	AR052610	Sequence	25
LOCUS	AR052610	AR052610	17 bp	DNA	linear	PAT 29-SEP-1999		
DEFINITION	Sequence 8 from patent US 5831066.							
ACCESSION	AR052610							
VERSION	AR052610.1	GI:5975974						
KEYWORDS								
SOURCE	Unknown.							
ORGANISM	Unclassified.							
REFERENCE	1 (bases 1 to 17)							
AUTHORS	Reed, J.C.							
TITLE	Regulation of bcl-2 gene expression							
JOURNAL	Patent: US 5831066-A 8 03-NOV-1998;							
FEATURES	Location/Qualifiers							
source	1..17							
BASE COUNT	1 a 7 c 5 g 4 t							
ORIGIN								

ALIGNMENTS

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C 44	11.2	65.9	50	6	AR148432	
C 43	11.2	65.9	50	6	AR045154	
C 42	11.2	65.9	50	6	AR160483	
C 41	11.2	65.9	37	6	AR075081	
C 40	11.2	65.9	37	6	AR075081	
C 39	11.2	65.9	33	6	AR069952	
C 38	11.2	65.9	28	6	E37205	Mouse secre
C 37	11.2	65.9	24	6	BD010808	Novel pol
C 36	11.2	65.9	21	6	AX000983	Sequence
C 35	11.2	65.9	21	6	AR084992	Sequence
C 34	11.2	65.9	21	6	AR053970	Sequence
C 33	11.2	65.9	21	6	AA2054	Sequence
C 32	11.2	65.9	20	6	BD004560	Fatty aci
C 31	11.4	67.1	75	3	HYDCNHV2	Sequence
C 30	11.4	67.1	34	6	A50157	Sequence
C 29	11.4	67.1	34	6	A49730	Sequence
C 28	11.4	67.1	33	6	A14926	Oligonucleo
C 27	11.4	67.1	31	6	AX179386	Sequence
C 26	11.4	67.1	30	6	A50153	Sequence
C 25	11.4	67.1	30	6	AX292017	Sequence
C 24	11.4	67.1	24	6	AX291629	Sequence
C 23	11.4	67.1	24	6	AX296650	Sequence
C 22	11.4	67.1	20	6	AX296650	Sequence
C 21	11.4	67.1	20	6	AX296650	Sequence
C 20	11.8	69.4	72	6	AX150235	Sequence
C 19	11.8	69.4	51	6	AX157607	Sequence
C 18	11.8	69.4	30	6	E49675	Insect cell
C 17	11.8	69.4	24	6	AX291094	Sequence
C 16	11.8	69.4	20	6	AX295727	Sequence
C 15	11.8	69.4	18	6	AR106803	Sequence
C 14	12.2	71.8	66	14	SHU29127	Suid herpes
C 13	12.2	71.8	31	6	I72670	Sequence
C 12	12.2	71.8	31	6	I72668	Sequence
C 11	12.2	71.8	31	6	I24849	Sequence
C 10	12.2	71.8	31	6	I24847	Sequence
C 9	12.8	75.3	45	6	A63054	Sequence
C 8	82.4	17	6	AR052611	Immunost	
C 7	15	88.2	18	6	BD009122	Sequence
C 6	15	88.2	18	6	AX355457	Sequence
C 5	15	88.2	18	6	AX103864	Sequence
C 4	15	88.2	18	6	AX103812	Sequence
C 3	15	88.2	18	6	AR154731	Sequence
C 2	15	88.2	18	6	AR146348	Sequence
C 1	100.0	17	6	AR052610	Sequence	

Query Match 100.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 96;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctctg 17
|||||
Db 1 CGCGTGCACCCCTCTG 17

RESULT 2
ARI46348
LOCUS ARI46348 18 bp DNA
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION ARI46348
VERSION ARI46348.1 GI:15109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using immunotherapeutic oligonucleotides and cytokines
JOURNAL Patent: US 6218371-A 60 17-APR-2001;
FEATURES Location/Qualifiers
Source 1..18
/organism="unknown"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 3
ARI54731
LOCUS ARI54731 18 bp DNA
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION ARI54731
VERSION ARI54731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
FEATURES Location/Qualifiers
Source 1..18
/organism="unknown"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 4
AX103812
LOCUS AX103812 18 bp DNA
DEFINITION Sequence 4 from Patent WO0122972.
ACCESSION AX103812

VERSION AX103812.1 GI:13920009
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
Source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 5
AX103864
LOCUS AX103864 18 bp DNA
DEFINITION Sequence 56 from Patent WO0122972.
ACCESSION AX103864
VERSION AX103864.1 GI:13920061
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical GmbH (DE)
FEATURES Location/Qualifiers
Source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 88.2%; Score 15; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgacccctct 15
|||||
Db 4 CGCGTGCACCCCTCT 18

RESULT 6
AX355457
LOCUS AX355457 18 bp DNA
DEFINITION Sequence 485 from Patent WO0197843.
ACCESSION AX355457
VERSION AX355457.1 GI:18620125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.

TITLE Methods for enhancing antibody-induced cell lysis and treating

JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;

UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES

Location/Qualifiers

1. .18

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="Synthetic oligonucleotide-phosphorothioate backbone"

BASE COUNT

2 a 8 c 4 g 4 t

ORIGIN

Query Match

88.2%; Score 15; DB 6; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtcgaccctct 15

|||||

Db 4 CGCGTCCGACCTCT 18

RESULT 7

BD009122 18 bp DNA linear PAT 31-JAN-2002

LOCUS Immunostimulatory nucleic acid molecules.

DEFINITION BD009122.1 GI:18637495

VERSION JP 2001503267-A/74.

KEYWORDS JP 2001503267-A/74.

SOURCE synthetic construct.

ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 18)

Krieg, A.M. and Kline, D.N.

Immunostimulatory nucleic acid molecules

Patent: JP 2001503267-A 74 13-MAR-2001;

JOURNAL UNIVERSITY OF IOWA RESEARCH FOUNDATION

COMMENT OS Artificial Sequence

PN JP 2001503267-A/74

PD 13-MAR-2001

PR 30-OCT-1997 JP 1998520784

PI 30-OCT-1996 US 08/738652

PC ARTHUR M KRIEG, JOEL N KLINE

PC C07H21/00, C07H21/02, C07H21/04, A61K31/175, A61K31/335, A61K31/47,

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

CC A61K31/70

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)

AUTHORS Reed, J.C.

JOURNAL Regulation of bcl-2 gene expression

Patent: US 5831066-A 9 03-NOV-1998;

FEATURES Location/Qualifiers

source 1. .17

BASE COUNT

2 a 8 c 4 g 3 t

ORIGIN

Query Match

82.4%; Score 14; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.9e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtcgaccctct 14

|||||

Db 4 CGCGTCCGACCTCT 17

RESULT 9

A63054/C

LOCUS A63054

DEFINITION Sequence 25 from Patent WO9718308.

ACCESSION A63054

VERSION A63054.1 GI:3716918

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 45)

Ashcroft, F., Sakura, H., Ashfield, R. and Ashcroft, S.J.

K-ATP CHANNEL PROTEIN AND METHODS RELATING TO IT

Patent: WO 9718308-A 25 22-MAY-1997;

WELLCOME TRUST LIMITED AS TRUS (GB)

COMMENT Other publication AU 7583296 19970605.

FEATURES Location/Qualifiers

source 1. .45

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT

11 a 18 c 7 g 9 t

ORIGIN

Query Match

75.3%; Score 12.8; DB 6; Length 45;

Best Local Similarity 87.5%; Pred. No. 2.1e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ggcgtcgaccctctg 17

|||||

Db 23 GGGTGGACCTCTG 8

RESULT 10

LOCUS I24847

DEFINITION Sequence 18 from patent US 5545816.

ACCESSION I24847

VERSION I24847.1 GI:1604717

KEYWORDS

SOURCE

ORGANISM

REFERENCE 1 (bases 1 to 31)

Ausich, R.L., Brinkhaus, F.L., Mukharji, I., Proffitt, J., Yarger, J.

phytoene biosynthesis in genetically engineered hosts

Patent: US 5545816-A 18 13-AUG-1996;

JOURNAL Location/Qualifiers

FEATURES

/gene="gC"
/note="formerly named glycoprotein III; signal peptide
mutant: Allele: del10"
/codon_start=1
/product="glycoprotein C"
/protein_id="AAC54537.1"
/db_xref="GI:902040"
/translation="MASLARMLLALYAAIAAAP"

BASE COUNT 4 a 27 c 24 g 11 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 14; Length 66;
Best Local Similarity 82.4%; Pred. No. 4.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

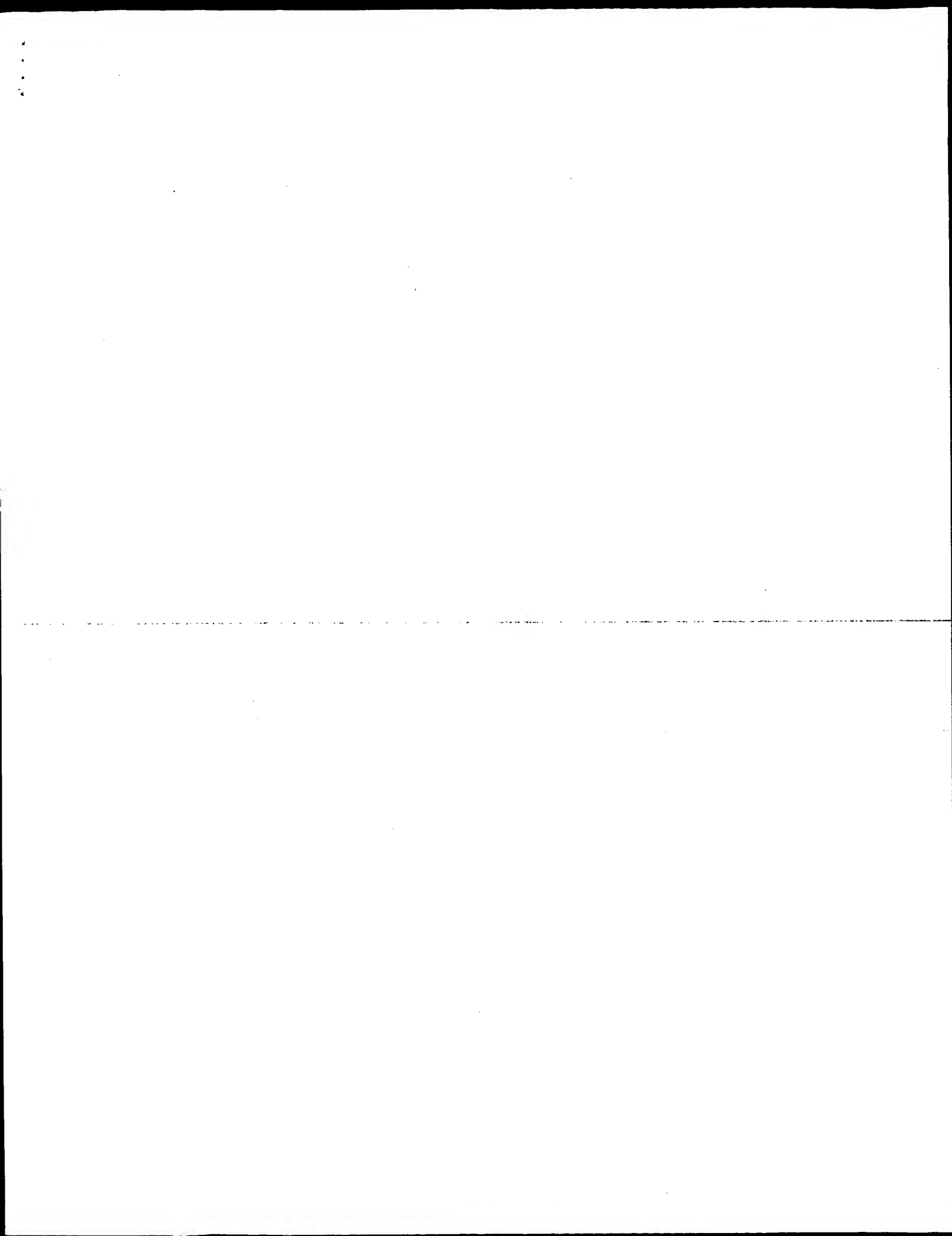
OY 1 cgcgtcgaccctcttg 17
||||| 11 11
Db 14 CGCGTGCATGCTCTG 30

RESULT 15
ARI06803 18 bp DNA linear PAT 14-FEB-2001
LOCUS ARI06803
DEFINITION Sequence 51 from patent US 6107091.
ACCESSION ARI06803
VERSION ARI06803.1 GI:12821333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsett,L.M.
TITLE Antisense Inhibition of G-alpha-16 expression
JOURNAL Patent: US 6107091-A 51 22-AUG-2000;
FEATURES
source 1..18
BASE COUNT 1 a 7 c 4 g 6 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 8.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 cgtgcgaccctcttg 17
||||| 11 11
Db 3 CGTGGCCCTCTTG 17

Search completed: June 28, 2002, 22:11:05
Job time: 8356 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:10 : Search time 1381.16 Seconds
(without alignments)
21.133 Million cell updates/sec

Title: US-09-709-170A-8

Perfect score: 17

Sequence: 1 cgcgtgcgacctctctg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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- 9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	AA086650	Bcl-2 antisense ol
2	17	100.0	17	AAV28172	Antisense Oligonuc
3	17	100.0	17	AAV23684	Deletion sequence
4	17	100.0	17	AAV18693	Target bcl-2 antis
5	15.4	90.6	20	AAH48722	Proto-oncogene bcl
6	15	88.2	18	AAV52546	Unmethylated CpG d
7	15	88.2	18	AAV27720	Immunostimulatory
8	15	88.2	18	AAV41906	IL-12 secretion in
9	15	88.2	18	AAV47644	Parasitic infectio

10	15	88.2	18	AAZ47982	Immune remodeling
11	15	88.2	18	AAH50628	Natural killer cel
12	15	88.2	18	AAV98888	Immunostimulatory
13	15	88.2	18	AAV98931	Immunostimulatory
14	14	85.3	17	AA086651	Bcl-2 antisense ol
15	12.8	75.3	45	AAV67093	K-ATP channel subu
16	12.2	71.8	31	AAV91550	Geranylgeranyl pyr
17	12.2	71.8	51	AAV28453	Human SNP oligonuc
18	11.8	69.4	18	AAA48801	Human G-alpha-16 a
19	11.8	69.4	18	AAH27725	Control oligonucle
20	11.8	69.4	20	AAV201955	PCR primer used to
21	11.8	69.4	20	AAV195769	Capture oligonucle
22	11.8	69.4	24	AB188108	Capture oligonucle
23	11.8	69.4	24	AB188109	Capture oligonucle
24	11.8	69.4	20	AAV14650	PCR primer for DNA
25	11.8	69.4	51	AAV73994	Human silent SNP c
26	11.8	69.4	72	AAV61882	Maize invertase DN
27	11.4	67.1	20	AAV62342	Human CS198 DNA pr
28	11.4	67.1	20	AAV62344	Human CS198 DNA pr
29	11.4	67.1	20	AAV13645	Human CS 198 EST-s
30	11.4	67.1	20	AAV13647	Human CS 198 EST-s
31	11.4	67.1	20	AAV196304	Capture oligonucle
32	11.4	67.1	20	AB196692	Capture oligonucle
33	11.4	67.1	24	AB189178	Capture oligonucle
34	11.4	67.1	24	AB189179	Capture oligonucle
35	11.4	67.1	24	AB189954	Capture oligonucle
36	11.4	67.1	24	AB189955	Capture oligonucle
37	11.4	67.1	26	AAV10806	PCR primer #1 spec
38	11.4	67.1	30	AAV14938	Mutant IL-1 recept
39	11.4	67.1	30	AAV130155	Interleukin-1 rece
40	11.4	67.1	31	AAV85333	5' PCR primer used
41	11.4	67.1	34	AAV14940	Mutant IL-1 recept
42	11.4	67.1	34	AAV30160	Interleukin-1 rece
43	11.4	67.1	14	AAV38042	Oligonucleotide Bt
44	11.4	67.1	61	AAV38043	Oligonucleotide Bt
45	11.4	67.1	71	AAV29094	Human secreted pro

ALIGNMENTS

RESULT 1	AA086650 standard; DNA; 17 BP.
ID	AA086650;
XX	27-SEP-1995 (first entry)
AC	Bcl-2 antisense oligonucleotide.
XX	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX	Lymphoma; programmed cell death; ss.
XX	Synthetic.
OS	
XX	Key
XX	misc-feature
XX	location/Qualifiers
XX	1..17
XX	/tag= a
XX	/note= "3'-5' (antisense) sequence"
XX	WO9508350-A.
XX	30-MAR-1995.
XX	20-SEP-1994; 94MO-US10725.
XX	20-SEP-1993; 93US-0124256.
XX	(REED/) REED J C.
XX	Reed JC;
XX	

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086550-55) or the 5'-cap
CC region (AA086556-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtcgagaccctcttg 17
Db 1 cgcgtcgagaccctcttg 17
|||||

RESULT 2
AAV28172
ID AAV28172 standard; DNA; 17 BP.
XX
AC AAV28172;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KW Purification; oligonucleotide; matrix; affinity unit;
KW affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9627425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US3284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Sriwatsa GS;
XX
DR WPI; 1998-362922/31.
XX
PT Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 79; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtcgagaccctcttg 17
Db 1 cgcgtcgagaccctcttg 17
|||||

RESULT 3
AAV23684
ID AAV23684 standard; DNA; 17 BP.
XX
AC AAV23684;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 137.
XX
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Sriwatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 149; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-x23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctctg 17
|||||
Db 1 cgcgtgcgacctctg 17

RESULT 4

AAHX18693
ID AAHX18693 standard; DNA; 17 BP.

AC AAHX18693;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #25.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;
KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
KW HIV; inflammation; ss.

XX Synthetic.

OS WO9901579-A1.

PN 14-JAN-1999.

PD 01-JUL-1998; 98WO-US13574.

PR 01-JUL-1997; 97US-0886829.

PA (ISIS-) ISIS PHARM INC.

PI Hardee G, Teng C;

DR WPI; 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used
PT particularly for delivering therapeutic antisense oligonucleotides
PT across the gastrointestinal mucosa, provides high bioavailability

PS Example 2; Page 84; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35,%. The penetration enhancer improves: (1) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAHX18693 to AAHX18799 and AAHX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.

XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctctg 17
|||||
Db 1 cgcgtgcgacctctg 17

RESULT 5

AAHA8722
ID AAHA8722 standard; DNA; 20 BP.

AC AAHA8722;

DT 19-OCT-2001 (first entry)

DE Proto-oncogene bcl-2 associated primer SEQ ID 3.

XX Primer; phosphorothioate; somatostatin; cytostatic; virucide; asthma;

KW antiinflammatory; antiasthmatic; cardiant; antisense therapy;
KW cancer; viral disease; inflammatory process; somatostatin receptor;
KW central nervous system disease; cardiovascular disease; SSTR;

KW proto-oncogene; bcl-2; ss.

XX Unidentified.

XX Key Location/Qualifiers

FT modified_base 1..20
FT /tag= a
FT /mod_base= "OTHER"
FT /note= "phosphorothioate"

PN DE10006572-A1.

PD 23-AUG-2001.

PE 14-FEB-2000; 2000DE-1006572.

PR 14-FEB-2000; 2000DE-1006572.

PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Eisenhut M, Mier W, Ertlla R, Haberkorn U;

DR WPI; 2001-530596/59.

XX New conjugates of oligonucleotides with somatostatin analogs, useful in
PT antisense therapy, e.g. of viral, inflammatory or asthmatic disease or
PT especially tumors overexpressing the somatostatin receptor -

PS Example 3; Page 9; 16pp; German.

XX This invention describes a novel oligonucleotide conjugate (I) comprising
CC (a) an oligonucleotide, at least part of the sequence of which is
CC complementary to part of an intracellular nucleic acid sequence; and (b)
CC a somatostatin analog. The products of the invention have cytostatic,
CC virucide, antiinflammatory, antiasthmatic and cardiant activity. The use
CC of (I) is claimed in antisense therapy, especially of cancer, viral
CC disease, inflammatory processes or asthmatic, central nervous system or
CC cardiovascular disease. (I) are especially used for therapy of tumors
CC overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung
CC tumors, breast tumors, brain tumors or other endocrine tumors), but are
CC also useful for treating viral diseases (e.g. herpes simplex-1
CC infection), inflammatory disease (typical target RNA the NF-Kappa-B),
CC asthmatic disease (typical target RNA the adenosine A1 receptor), central
CC nervous system disease (typical target RNA the dopamine receptor) or
CC cardiovascular disease (typical target RNA c-myc). (I) are efficiently
CC taken up by cells and incorporated in target cells (via the SSTR) and are
CC highly selective for cells overexpressing SSTRs. This sequence
CC represents a primer used to illustrate the method of the invention.

XX Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 20;
Best Local Similarity 94.1%; Pred. No. 39;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 cgcgtgcgacctctg 17
|||

Db 4 cgtgtgcgacctctg 20

RESULT 6
AAV52546
ID AAV52546 standard; DNA; 18 BP.

XX AAV52546;

XX 20-NOV-1998 (first entry)

DE Unmethylated Cpg dinucleotide 1761.

XX Unmethylated Cpg dinucleotide; immune response; bacterial meningitis;

KW natural killer cell activation; NK cell; Th2 response; neonatal sepsis;

KW pulmonary disorder; asthma; environmentally induced airway disease;

KW bacterial infection; endotoxaemia; therapy; cystic fibrosis;

XX inflammatory bowel disease; ss.

XX Synthetic.

OS WO9837919-A1.

XX 03-SEP-1998.

XX 25-FEB-1998; 98WO-US03678.

XX 28-FEB-1997; 97US-0039405.

XX (IOWA) UNIV IOWA RES FOUND.

XX Krieg AM, Schwartz DA;

XX WPI; 1998-480941/41.

XX Use of nucleic acids containing an unmethylated Cpg - for treating a

XX subject having or at risk of having an acute decrement in air flow

XX or inhibiting an inflammatory response

XX Example 4; Page 35; 65pp; English.

XX This sequence represents an unmethylated Cpg dinucleotide, and can be

XX used in the method of the invention. The method is for treating a subject

XX having, or at risk of having an acute decrement in air flow, comprising

XX administering a nucleic acid sequence containing at least one

XX unmethylated Cpg. The nucleic acid contains an unmethylated Cpg

XX dinucleotide affect an immune response in a subject by activating natural

XX killer cells (NK) or redirecting a subject's immune response from a Th2

XX to a Th1 response by inducing monocytic and other cells to produce Th1

XX cytokines. They can be used to treat pulmonary disorders having an

XX immunologic component, such as asthma or environmentally induced airway

XX disease. They can also be used to treat diseases associated with

XX Gram-positive bacterial infections or endotoxaemia including bacterial

XX meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease

XX and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal

XX abscess, haemorrhagic shock, disseminated intravascular coagulation, or

XX an inflammatory response to lipopolysaccharide.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

SQ

Query Match 88.2%; Score 15; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctct 15

DB 4 cgcgtgcgacctct 18

RESULT 7
AAV27720
ID AAV27720 standard; DNA; 18 BP.

XX AAV27720;

XX 01-OCT-1998 (first entry)

DE Immunostimulatory oligodeoxyribonucleotide of the invention.

XX Immunostimulatory; oligodeoxyribonucleotide; ODN;

KW unmethylated Cpg dinucleotide; activate; lymphocyte; immune response;

KW Th2; cytokine; treatment; prevention; asthma; autoimmune disease;

KW desensitisation therapy; artificial adjuvant; antibody generation; ss.

XX Synthetic.

OS WO9818810-A1.

XX 07-MAY-1998.

XX 30-OCT-1997; 97WO-US19791.

XX 30-OCT-1996; 96US-0738652.

XX (IOWA) UNIV IOWA RES FOUND.

XX Kline JN, Krieg AM;

XX WPI; 1998-272127/24.

XX New immunostimulatory nucleic acid molecules - which contain at

XX least one unmethylated Cpg dinucleotide, used for treating e.g.

XX tumours, infections or autoimmune disease

XX Disclosure; Page 49; 109pp; English.

XX AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides

XX (ODNs) of the invention. The ODNs contain at least one unmethylated Cpg

XX dinucleotide, and have the formula:

XX 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive

XX Cpgs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N

XX is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and

XX N2 does not contain a CCGG tetramer or more than one CCG or CGG trimer

XX OR 5' NX1X2CGX3X4N 3', where at least one nucleotide separates

XX consecutive Cpgs, X1 and X2 are selected from GpT, GpG, GpA, ApT and ApA,

XX X3 and X4 are selected from Tpt or Cpt, N is any nucleotide and N1+N2 is

XX 0-26 bases with the provision that N1 and N2 does not contain a CCGG

XX tetramer or more than one CCG or CGG trimer.

XX The ODNs activate lymphocytes in a subject and redirect a subject's

XX immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells

XX and other cells to produce Th1 cytokines, including IL-12, IFN-gamma and

XX GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,

XX autoimmune diseases, in desensitisation therapy, as an artificial

XX adjuvant during antibody generation in a mammal such as a mouse or a

XX human.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

SQ

Query Match 88.2%; Score 15; DB 19; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctct 15

DB 4 cgcgtgcgacctct 18

RESULT 8
AAZ41906
ID AAZ41906 standard; DNA; 18 BP.

XX AAZ41906;

XX 24-JAN-2000 (first entry)

XX IL-12 secretion inducing Cpg oligonucleotide 51.
DE Cpg oligonucleotide; phosphorothioate; interleukin-12; IL-12; secretion;
XX human PBMC; immune response; cancer; HIV; bacterial disease; asthma;
KW neoplastic disorder; jaagsiekte; B cell; NK cell; ss; cytokine;
KW antigen presenting cell; infection; allergic disease.
XX
OS Synthetic.
XX
PN WO951259-A2.
XX
PD 14-OCT-1999.
XX
PF 02-APR-1999; 99WO-US07335.
XX
PR 03-APR-1998; 98US-0080729.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Krieg AM, Weiner G;
XX
PI MPI; 1999-620169/53.
XX
PT Novel synergistic combinations of immunostimulatory oligonucleotides
PT and immunopotentiating cytokines are useful for stimulating the immune
PT system -
XX
PS Example 8; Page 80; 91pp; English.
XX
SQ Sequences AA241856-241949 are phosphorothioate Cpg oligonucleotides
XX which are used in the invention to induce interleukin-12 (IL-12)
CC secretion from human PBMC. The invention comprises stimulating an immune
CC response in a subject comprising administering to a subject exposed to an
CC antigen, an immunopotentiating cytokine and an immunostimulatory Cpg
CC oligonucleotide to induce a synergistic antigen specific immune
CC response. The methods are useful for treating cancer by stimulating an
CC antigen specific immune response against a cancer antigen. The methods
CC can also be used to treat neoplastic disorders in humans, including but
CC not limited to: sarcoma, carcinoma, fibroma, lymphoma, melanoma,
CC neuroblastoma, retinoblastoma, and glioma. The methods are also useful
CC for treating infectious diseases, e.g. viral diseases such as HIV,
CC bacterial diseases, and fungal diseases. The methods may also be used to
CC treat allergic diseases, e.g. asthma. The methods and compositions may
CC also be applied to treat cancer and tumours in non human subjects,
CC e.g. cats and dogs. Neoplasias affecting agricultural livestock may also
CC be treated and include leukaemia, haemangioendothelioma and bovine ocular
CC neoplasia. Chronic, infectious, contagious diseases of sheep and goats
CC caused by the bacterium *Corynebacterium pseudotuberculosis*, and
CC contagious lung tumour of sheep caused by jaagsiekte may also be
CC treated. Cpg oligonucleotides can be useful in activating B cells, NK
CC cells, and antigen presenting cells, such as monocytes and macrophages.
CC Cpg oligonucleotides enhance antibody dependent cellular cytotoxicity and
CC can be used as an adjuvant in conjunction with tumour antigens to
CC protect against a tumour challenge.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgaccctct 15
|||||
DB 4 cgcgtgcgaccctct 18

RESULT 9
AA247644
ID AA247644 standard; DNA; 18 BP.
XX
AC AA247644;

XX 01-MAR-2000 (first entry)
DE Parasitic infection preventing exemplary oligonucleotide SEQ ID NO:50.
XX
KW Immune system; immunostimulatory; parasitic infection; parasite;
KW Cpg oligonucleotide; antigen presenting cell; natural killer cell;
KW granulocyte; malaria; helminth disease; tick; mite; ss.
XX
OS Synthetic.
XX
PN WO956755-A1.
XX
PD 11-NOV-1999.
XX
PF 06-MAY-1999; 99WO-US09863.
XX
PR 06-MAY-1998; 98US-0084512.
XX
PA (IOWA) UNIV IOWA RES FOUND.
PA (OTTA-) OTTAWA CIVIC LOEB RES INST.
PA (USNA) US SEC OF NAVY.
XX
PI Gramzinski RA, Krieg AM, Davis HL, Hoffman SL;
XX
PI MPI; 2000-062123/05.
XX
PT Treating and preventing parasitic infections using Cpg oligonucleotides
PT
XX
PS Disclosure; Page 20; 74pp; English.
XX
SQ The present invention describes a method for treating and preventing
XX parasitic infection by administration of unmethylated Cpg
XX oligonucleotides. The Cpg oligonucleotides are able to stimulate the
XX innate immune system via the activation of immune cells, such as antigen
XX presenting cells, natural killer cells and granulocytes. The Cpg
XX oligonucleotides and the method can be used to treat and prevent
XX parasitic diseases, such as malaria, helminth diseases, tick and mites
XX in humans, animals and poultry. The oligonucleotides may be administered
XX in conjunction with parasitocides or other therapeutic compounds after
XX an organism has been diagnosed to be infected with parasites. Diseases
XX which can be treated or prevented include those caused by *Plasmodium*
XX *falciparum*, *P. ovale*, *P. malariae*, *P. vivax*, *P. knowlesi*, *Babesia*
XX *microti*, *B. divergens*, *Trypanosoma cruzi*, *T. gambiense*, *T. rhodesiense*,
XX *Schistosoma mansoni*, *Toxoplasma gondii*, *Trichinella spiralis*, *Leishmania*
XX *major*, *L. donovani*, *L. braziliensis*, and *L. tropica*. The parasite is
XX especially capable of causing malaria. The present sequence represents
XX a parasitic infection preventing exemplary oligonucleotide sequence from
XX the present invention.
XX
SQ Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgaccctct 15
|||||
DB 4 cgcgtgcgaccctct 18

RESULT 10
AA247982
ID AA247982 standard; DNA; 18 BP.
XX
AC AA247982;
XX
XX 08-MAR-2000 (first entry)
DE Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:60.
XX
KW Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;

KW immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
KW immune response; allergic reaction; infectious disease; asthma;
KW thrombocytopaenia; immunohaemolytic disorder; genetic disorder;
KW hemoglobinopathy; kidney failure; chronic inflammatory disorder;
KW rheumatoid arthritis; ss.

OS Synthetic.

PN WO9558118-A2.

XX 18-NOV-1999.

PD 14-MAY-1999; 99WO-IB01285.

PF 14-MAY-1998; 98US-0085516.

PR 02-FEB-1999; 99US-0241653.

XX (CPGT-) CPG IMMUNOPHARMACEUTICALS GMBH.

PA (CPGT-) CPG IMMUNOPHARMACEUTICALS INC.

PI Wagner H, Lipford G;

DR WPI; 2000-062261/05.

XX Use of CPG containing oligonucleotides for, e.g. inducing an

PT antigen-specific immune response

XX Example 1; Page 66; 116pp; English.

CC The present invention describes a method using CPG containing
CC oligonucleotides (ONS) for regulating immune system remodeling and for
CC regulating haematopoiesis. The method for inducing an antigen-specific
CC immune response comprises: (1) administering an ON having a sequence
CC including at least the formula (1); and (2) exposing the subject to an
CC antigen at least 3 days after the ON is administered to the subject to
CC produce an antigen-specific immune response: 5' X1CXX2 3' (1), where
CC the ON = includes at least 8 nucleotides; C and G = unmethylated, and
CC X1 and X2 = nucleotides. The method can be used for inducing an immune
CC response against an antigen such as cells, cell extracts, proteins,
CC polysaccharides, polysaccharide conjugates, lipids, glycolipids,
CC carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
CC allergens. It can be used in a subject at risk of developing cancer or
CC an allergic reaction. It can also be used for treating an infectious
CC disease, allergic diseases and asthma, as well as thrombocytopaenia
CC which is drug-induced, due to an autoimmune disorder such as idiopathic
CC thrombocytopenic purpura, or resulting from accidental or therapeutic
CC radiation exposure. It can also be used for treating anaemia such as
CC drug-induced anaemia, immunohaemolytic disorder, genetic disorders such
CC as haemoglobinopathy and inherited haemolytic anaemia, inadequate
CC production despite adequate iron stores, chronic disease such as kidney
CC failure, and chronic inflammatory disorder such as rheumatoid arthritis,
CC or anaemia resulting from accidental or therapeutic radiation exposure.
CC AA47932 to AA478029 represent phosphorothioate CPG oligonucleotides
CC used in the exemplification of the present invention.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

SO Query Match 88.2%; Score 15; DB 21; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 cgcgtgcgacctct 15

Db 4 cgcgtgcgacctct 18

RESULT 11

AAH50628

ID AAH50628 standard; DNA; 18 BP.

XX AC AAH50628;

XX

DT 22-AUG-2001 (first entry)

XX Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:60.

DE Immunostimulatory; inducing; natural killer cell; lytic activity;

XX unmethylated CPG dinucleotide; immune response; B cell proliferation;

KW Th1; immune activation; interleukin 6; IL-6; interferon gamma;

KN IFN-gamma; cytokine; ss.

XX Homo sapiens.

OS Synthetic.

PN US629116-B1.

XX 29-MAY-2001.

PD 30-OCT-1997; 97US-0960774.

PF 30-OCT-1996; 96US-0738652.

PR (IOWA) UNIV IOWA RES FOUND.

XX (COLE-) COLEY PHARM GROUP INC.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Krieger AM, Kline JN;

PI WPI; 2001-380456/40.

DR Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating

XX natural killer cell lytic activity in a human, comprise administering

PT to the subject or exposing a natural killer cell to immunostimulatory

XX nucleic acids

PS Disclosure; Column 32; 74pp; English.

CC The present invention describes methods for inducing interleukin 6
CC (IL-6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating
CC natural killer cell lytic activity. The methods comprise administering
CC to the subject or exposing a natural killer cell to an immunostimulatory
CC nucleic acid. Also described are: (1) inducing IL-6 in a subject
CC comprising administering to the subject to induce IL-6 in a subject
CC the immunostimulatory nucleic acid; (2) stimulating natural killer cell
CC lytic activity comprising exposing a natural killer cell to the
CC immunostimulatory nucleic acid to stimulate natural killer cell lytic
CC activity; (3) inducing interferon-gamma in a subject to treat an immune
CC system deficiency comprising administering to the subject to induce
CC interferon-gamma production, the immunostimulatory nucleic acid; and
CC (4) inducing IL-12 in a subject comprising administering to the subject
CC the immunostimulatory nucleic acid. The methods are useful for inducing
CC IL-6, interferon-gamma or IL-12, or stimulating natural killer cell
CC lytic activity in a subject, particularly a human. The methods are
CC particularly useful for modulating an immune response. AAH50571 to
CC AAH50671 represent oligonucleotide sequences used in the exemplification
CC of the present invention.

XX Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

SO Query Match 88.2%; Score 15; DB 22; Length 18;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 cgcgtgcgacctct 15

Db 4 cgcgtgcgacctct 18

RESULT 12

AAF98888

ID AAF98888 standard; DNA; 18 BP.

XX AC AAF98888;

XX


```

XX      A DNA probe (AA167093) is based on the 3' untranslated region of the
CC      mouse K-ATP channel Kir6.2 gene (see also AA167087), starting at
CC      mouse K-ATP channel Kir6.2 gene (see also AA167087), starting at
CC      nucleotide +85. Probes (AA167092-93) based on Kir6.2 and SUR1
CC      sequences were used for in-situ hybridisation analysis of samples
CC      from adult rat and mouse brain sections. The probes were designed
CC      for least similarity to other subfamily members to minimise
CC      cross-hybridisation. The results indicated the the brain K-ATP
CC      channel has Kir6.2 (see also AA167931-32) and SUR1 subunits.
XX
S0      Sequence 45 BP; 11 A; 18 C; 7 G; 9 T; 0 other;

Query Match          75.3%; Score 12.8; DB 18; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 gcgtgcagacctcttg 17
      | ||||| |||||
Db      23 GGGTGCACAGCCTCTTG 8

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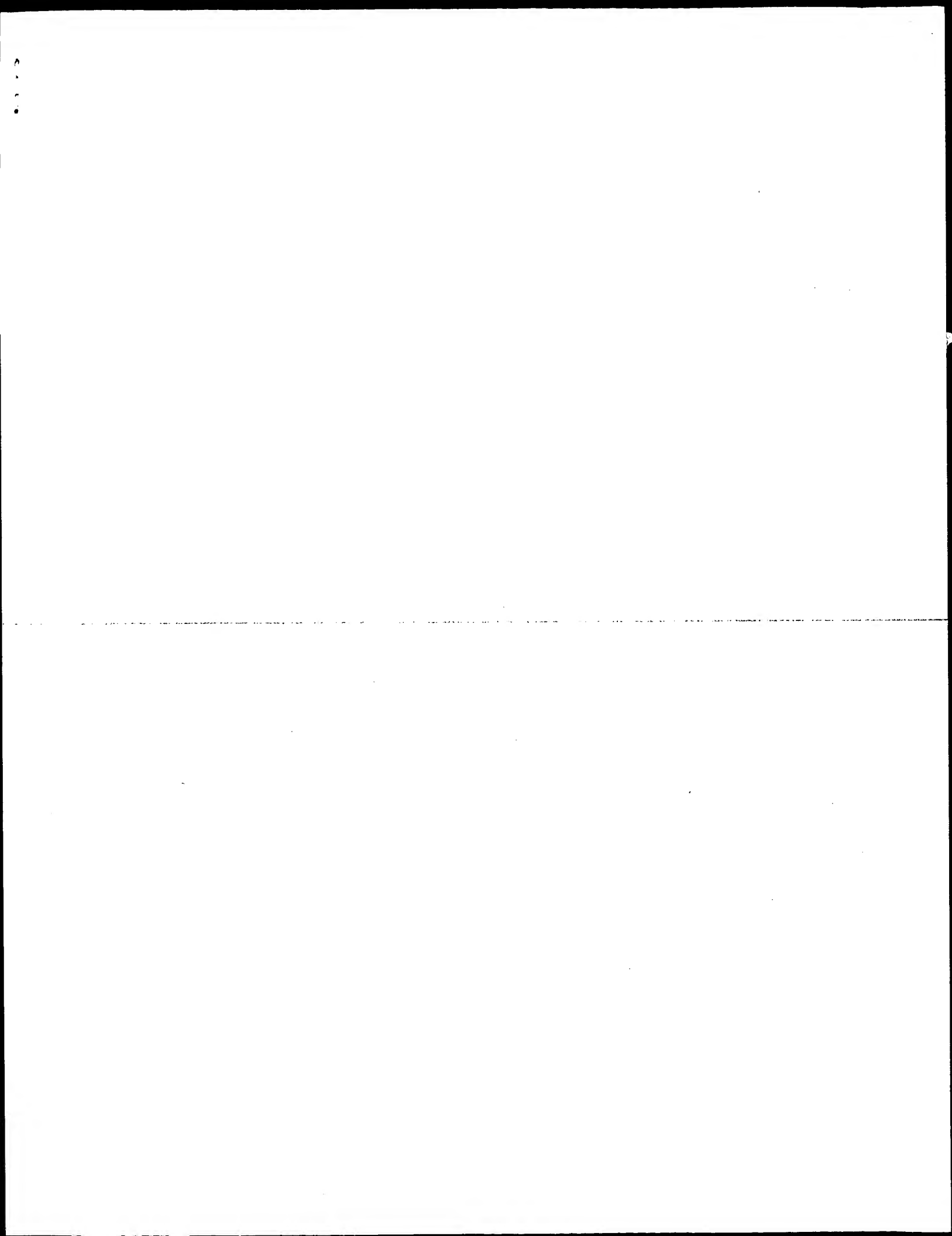
Query Match          75.3%; Score 12.8; DB 18; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.le+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 gcgtgcgacctcttg 17
        | | | | | | | | | |
Db       23 GGGTGCAGCCTCTTG 8

```

Mon Jul 1 08:41:00 2002

us-09-709-170a-8.szlm75.rng



GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run On: June 28, 2002, 22:16:45 : Search time 334.55 Seconds
(Without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-8

Perfect score: 17

Sequence: 1 cgcgtgcagacctctg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCITUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	2	US-08-465-485A-8
2	17	100.0	17	3	US-09-080-285-8
3	15	88.2	18	4	US-09-030-701-28
4	15	88.2	18	4	US-09-286-098-60
5	15	88.2	18	4	US-08-960-774-60
6	14	82.4	17	2	US-08-465-485A-9
7	14	82.4	17	3	US-08-080-285-9
8	12.2	71.8	31	1	US-08-095-726-25
9	12.2	71.8	31	1	US-08-095-726-27
10	12.2	71.8	31	1	US-08-096-043-22
11	12.2	71.8	31	1	US-08-096-043-24
12	12.2	71.8	31	1	US-08-093-577-18
13	12.2	71.8	31	1	US-08-093-577-20
14	12.2	71.8	31	1	US-08-096-623A-30
15	12.2	71.8	31	1	US-08-096-623A-32
16	11.8	69.4	30	2	US-08-809-185-3
17	11.8	67.1	30	2	US-08-809-185-5
18	11.4	67.1	34	2	US-08-809-185-7
19	11.4	65.9	21	2	US-08-357-146-7
20	11.2	65.9	21	2	US-09-154-344-7
21	11.2	65.9	33	2	US-08-873-479-39
22	11.2	65.9	35	3	US-08-959-212-11
23	11.2	65.9	37	4	US-09-031-442A-7
24	11.2	65.9	37	4	US-09-258-377-7
25	11.2	65.9	50	1	US-08-137-117D-60
26	11.2	65.9	50	1	US-08-436-717-60
27	11.2	65.9	50	4	US-08-974-691-13

C	28	11.2	65.9	71	4	US-09-025-760B-95	Sequence 95, Appl
	29	11	64.7	17	2	US-08-465-485A-10	Sequence 10, Appl
	30	11	64.7	17	3	US-09-080-285-10	Sequence 10, Appl
C	31	11	64.7	17	4	US-08-584-040-7553	Sequence 7553, Ap
	32	11	64.7	67	4	US-09-025-769B-83	Sequence 83, Appl
C	33	10.8	63.5	21	4	US-08-943-731-266	Sequence 266, Ap
	34	10.8	63.5	24	2	US-08-859-998-1250	Sequence 1250, Ap
C	35	10.8	63.5	24	4	US-09-225-928-1250	Sequence 1250, Ap
	36	10.8	63.5	33	2	US-08-461-030C-5	Sequence 5, Appl
	37	10.8	63.5	33	3	US-08-744-138-12	Sequence 12, Appl
	38	10.8	63.5	33	4	US-09-241-376-12	Sequence 12, Appl
	39	10.8	63.5	33	5	PCT-US95-07135-5	Sequence 5, Appl
	40	10.8	63.5	49	1	US-08-171-389-43	Sequence 43, Appl
	41	10.8	63.5	49	1	US-08-123-936-43	Sequence 43, Appl
	42	10.8	63.5	49	2	US-08-475-228A-43	Sequence 43, Appl
	43	10.8	63.5	49	3	US-08-482-080A-43	Sequence 43, Appl
	44	10.8	63.5	49	5	PCT-US93-1238B-43	Sequence 43, Appl
C	45	10.8	63.5	54	1	US-08-373-124A-2236	Sequence 2236, Ap

ALIGNMENTS

RESULT 1
US-08-465-485A-8
Sequence 8, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: OHION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08465485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-8

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctcttg 17
|||||
DB 1 cgcgtgcgacctcttg 17

RESULT 2

US-09-080-285-8
; Sequence 8, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-8

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctcttg 17
|||||
DB 1 cgcgtgcgacctcttg 17

RESULT 3
US-09-030-701-28
; Sequence 28, Application US/09030701B
; Patent No. 6214806
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Schwartz, David A.
; TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
; TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
; FILE REFERENCE: C1039/77011
; CURRENT APPLICATION NUMBER: US/09/030,701B
; CURRENT FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/039,405
; PRIOR FILING DATE: 1997-02-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
; US-09-030-701-28

Query Match 88.2%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctt 15
|||||
DB 4 cgcgtgcgacctctt 18

RESULT 4
US-09-286-098-60
; Sequence 60, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Weiner, George
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; US-09-286-098-60

Query Match 88.2%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctt 15
|||||
DB 4 cgcgtgcgacctctt 18

RESULT 5

US-08-960-774-60
; Sequence 60, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieger et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-960-774-60

Query Match 88.2%; Score 15; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cgcgtgagacctc 15
|||||
Db 4 CGCGTGCACCTCT 18

RESULT 6
US-08-465-485A-9
; Sequence 9, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-9

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-9

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 cgcgtgagacctc 14
|||||
Db 4 CGCGTGCACCTCT 17

RESULT 7
US-09-080-285-9
; Sequence 9, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 14
|||||
DB 4 CGCGTCGCACCCCTC 17

RESULT 8

US-08-095-726-25
Sequence 25, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-25

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 17
|||||
DB 4 CGCATGCGACCTGTGTG 20

RESULT 9

US-08-095-726-27/c
Sequence 27, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Auslich, Rodney L
APPLICANT: Brinkhaus, Friedhelm L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Huel-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-095-726-27

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 17
|||||
DB 28 CGCATGCGACCTGTGTG 12


```
RESULT 10
US-08-096-043-22
; Sequence 22, Application US/08096043
; Patent No. 5530189
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Lycopen Biosynthesis in
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,043
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,568
; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5530189val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-096-043-22

Query Match          71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtcgaccctctg 17
   ||| ||| ||| ||| ||
Db 4 CGCATCGACCCCTGTG 20

RESULT 11
US-08-096-043-24/c
; Sequence 24, Application US/08096043
; Patent No. 5530189
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Lycopen Biosynthesis in
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
```

```
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096,043
; FILING DATE: 22-JUL-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,568
; FILING DATE: 30-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5530189val B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3128567180
; TELEFAX: 3128564972
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-096-043-24
```

```
Query Match          71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtcgaccctctg 17
   ||| ||| ||| ||| ||
Db 28 CGCATCGACCCCTGTG 12
```

```
RESULT 12
US-08-093-577-18
; Sequence 18, Application US/08093577
; Patent No. 5545816
; GENERAL INFORMATION:
; APPLICANT: Ausich, Rodney L
; APPLICANT: Brinkhaus, Friedhelm L
; APPLICANT: Mukharji, Indrani
; APPLICANT: Proffitt, John H
; APPLICANT: Yarger, James G
; APPLICANT: Yen, Huel-Che B
; TITLE OF INVENTION: Phytoene Biosynthesis in
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corp., Patents and Licensing Dept
; STREET: 200 E Randolph St
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60680-0703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,577
; FILING DATE: 19-JUL-1993
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/785,569
```

FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-093-577-18

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 17
||| ||||| ||
Db 4 CGCATGCGACCTTGTC 20

RESULT 13
US-08-093-577-20/c
Sequence 20, Application US/08093577
Patent No. 5545816
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Phytoene Biosynthesis in
NUMBER OF SEQUENCES: 43
TITLE OF INVENTION: Genetically Engineered Hosts
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,577
FILING DATE: 19-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,569
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5545816val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180
TELEFAX: 3128564972
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-093-577-20

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgtgcgacctctg 17
||| ||||| ||
Db 28 CGCATGCGACCTTGTC 12

RESULT 14
US-08-096-623A-30
Sequence 30, Application US/08096623A
Patent No. 5684238
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L.
APPLICANT: Brinkhaus, Friedhelm L.
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H.
APPLICANT: Yarger, James G.
APPLICANT: Yen, Huel-Che B.
TITLE OF INVENTION: Biosynthesis of Zeaxanthin and
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welsh & Katz, Ltd.
STREET: 120 S. Riverside Plaza, 22nd Floor
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/096,623A
FILING DATE: 22-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,061
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/662,921
FILING DATE: 28-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/562,674
FILING DATE: 03-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/525,551
FILING DATE: 18-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/487,613
FILING DATE: 02-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamson, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: AMO-006.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 655-1500
TELEFAX: (312) 655-1501
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-096-623A-30

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 cgcgcgcaccctcttg 17
||| ||||| ||
Db 4 CGCATGCGACCTTGTG 20

RESULT 15
US-08-096-623A-32/C

; Sequence 32, Application US/08096623A
; Patent No. 5684238

; GENERAL INFORMATION:

; APPLICANT: Ausich, Rodney L.

; APPLICANT: Brinkhaus, Friedhelm L.

; APPLICANT: Muharrij, Indrani

; APPLICANT: Profitit, John H.

; APPLICANT: Yarger, James G.

; TITLE OF INVENTION: Biosynthesis of zeaxanthin and

; NUMBER OF SEQUENCES: 104

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Welsh & Katz, Ltd.

; STREET: 120 S. Riverside Plaza, 22nd Floor

; CITY: Chicago

; STATE: IL

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/096,623A

; FILING DATE: 22-JUL-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/805,061

; FILING DATE: 09-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/662,921

; FILING DATE: 28-FEB-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/562,674

; FILING DATE: 03-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/525,551

; FILING DATE: 18-MAY-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/487,613

; FILING DATE: 02-MAR-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Gamson, Edward P.

; REGISTRATION NUMBER: 29,381

; REFERENCE/DOCKET NUMBER: AMO-006.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 655-1500

; TELEFAX: (312) 655-1501

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 31 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-096-623A-32

QY 1 cgcgtgcaccctcttg 17
||| ||||| ||
Db 28 CGCATGCGACCTTGTG 12

Search completed: June 28, 2002, 22:16:46
Job time: 8272 sec

Query Match 71.8%; Score 12.2; DB 1; Length 31;
Best Local Similarity 82.4%; Pred. No. 3,4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Mon Jul 1 08:41:00 2002

us-09-709-170a-8.szlm75.rn1

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:05 ; Search time 3762.88 seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170A-9

Perfect score: 17
Sequence: 1 taccgcgtgcaccctc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_bt: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
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29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description
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1	17	100.0	17	6	AR052611	AR052611 Sequence
2	17	100.0	18	6	AR146348	AR146348 Sequence
3	17	100.0	18	6	AR154731	AR154731 Sequence
4	17	100.0	18	6	AX103812	AX103812 Sequence
5	17	100.0	18	6	AX103864	AX103864 Sequence
6	17	100.0	18	6	AX355457	AX355457 Sequence
7	17	100.0	18	6	BD009122	BD009122 Sequence
8	14	82.4	17	6	AR052610	AR052610 Sequence
9	14	82.4	17	6	AR052612	AR052612 Sequence
10	13.8	81.2	24	6	BD010808	BD010808 Novel pol
11	12.8	75.3	51	6	AX162817	AX162817 Sequence
12	12.8	75.3	51	6	AX162819	AX162819 Sequence
13	12.8	75.3	18	6	E12821	E12821 Antisense o
14	11.8	69.4	18	6	E21868	E21868 Solid tumor
15	11.8	69.4	18	6	E21869	E21869 Solid tumor
16	11.8	69.4	20	6	AX296262	AX296262 Sequence
17	11.8	69.4	24	6	AX291629	AX291629 Sequence
18	11.4	67.1	31	6	AX179386	AX179386 Sequence
19	11.4	67.1	31	6	I24847	I24847 Sequence
20	11.4	67.1	31	6	I24849	I24849 Sequence
21	11.4	67.1	31	6	I72670	I72670 Sequence
22	11.4	67.1	31	6	I72670	I72670 Sequence
23	11.4	67.1	33	6	AX14926	AX14926 Oligonucleo
24	11.4	67.1	51	6	AX164886	AX164886 Sequence
25	11.2	65.9	19	6	AR152817	AR152817 Sequence
26	11.2	65.9	28	6	AR003376	AR003376 Sequence
27	11.2	65.9	28	6	I21165	I21165 Sequence
28	11.2	65.9	28	6	I74432	I74432 Sequence
29	11.2	65.9	32	6	AR153621	AR153621 Sequence
30	11.2	65.9	32	6	BD004220	BD004220 Liver fun
31	11.2	65.9	34	6	BD004224	BD004224 Liver fun
32	11.2	65.9	39	6	AX162310	AX162310 Sequence
33	11.2	65.9	44	6	I32830	I32830 Sequence
34	11.2	65.9	49	6	AX279745	AX279745 Sequence
35	11.2	65.9	51	6	AX158282	AX158282 Sequence
36	11.2	65.9	51	6	AX162808	AX162808 Sequence
37	11.2	65.9	51	6	AX162818	AX162818 Sequence
38	11.2	65.9	51	6	AX162820	AX162820 Sequence
39	11.2	65.9	55	6	AR101963	AR101963 Sequence
40	11.2	65.9	59	6	I32832	I32832 Sequence
41	11.2	65.9	59	12	SYNECOCVK	SYNECOCVK
42	11.2	65.9	69	6	AR101981	AR101981 Sequence
43	11.2	65.9	17	6	AR052613	AR052613 Sequence
44	11	64.7	6	6	A60774	A60774 Sequence
45	11	64.7	6	6	A60774	A60774 Sequence

ALIGNMENTS

RESULT 1
LOCUS AR052611 17 bp DNA
DEFINITION Sequence 9 from patent US 5831066.
ACCESSION AR052611
VERSION AR052611.1 GI:5975975
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;
FEATURES
SOURCE Location/Qualifiers
BASP COUNT: 2 a 8 c 4 g 3 t
ORIGIN

Query Match 100.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccggtgagaccctc 17
|||||
Db 1 TACCGCGTGGACCCCTC 17

RESULT 2
ARI46348
LOCUS ARI46348 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION ARI46348
VERSION ARI46348.1 GI:15109537
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
immunotherapeutic oligonucleotides and cytokines
JOURNAL Patent: US 6218371-A 60 17-APR-2001;
FEATURES
source 1..18
/organism="unknown"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 17; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccggtgagaccctc 17
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Db 1 TACCGCGTGGACCCCTC 17

RESULT 3
ARI54731
LOCUS ARI54731 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION ARI54731
VERSION ARI54731.1 GI:15122784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
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BASE COUNT 2 a 8 c 4 g 4 t
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Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccggtgagaccctc 17
|||||
Db 1 TACCGCGTGGACCCCTC 17

RESULT 4
AX103812
LOCUS AX103812 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 4 from Patent WO0122972.
ACCESSION AX103812

VERSION AX103812.1 GI:13920009
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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/db_xref="taxon:32630"
BASE COUNT 2 a 8 c 4 g 4 t
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Query Match 100.0%; Score 17; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccggtgagaccctc 17
|||||
Db 1 TACCGCGTGGACCCCTC 17

RESULT 5
AX103864
LOCUS AX103864 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 56 from Patent WO0122972.
ACCESSION AX103864
VERSION AX103864.1 GI:13920061
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccggtgagaccctc 17
|||||
Db 1 TACCGCGTGGACCCCTC 17

RESULT 6
AX355457
LOCUS AX355457 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 485 from Patent WO0197843.
ACCESSION AX355457
VERSION AX355457.1 GI:18620125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.

TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 485 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 17; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgctgcgaccctc 17
|||||
Db 1 TACCGCTGCGACCCCTC 17

RESULT 7
BD009122 18 bp DNA linear PAT 31-JAN-2002
LOCUS Immunostimulatory nucleic acid molecules.
DEFINITION BD009122
ACCESSION BD009122.1 GI:18637495
VERSION JP 2001503267-A/74.
KEYWORDS JP 2001503267-A/74.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kriegl, A.M. and Kline, J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: JP 2001503267-A 74 13-MAR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2001503267-A/74
PD 13-MAR-2001
PF 30-OCT-1997 JP 1998520784
PR 30-OCT-1996 US 08/738652
PI ARTHUR M KRIEGL, JOEL N KLINE
PC C07H21/00, C07H21/02, C07H21/04, A61K31/175, A61K31/335, A61K31/47,
PC A61K31/70
CC
FH Key Location/Qualifiers
FT source 1..18
FT Location/Qualifiers
1..18 /organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 17; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgctgcgaccctc 17
|||||
Db 1 TACCGCTGCGACCCCTC 17

RESULT 8
AR052610 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 8 from patent US 5831066.
DEFINITION AR052610
ACCESSION AR052610
VERSION AR052610.1 GI:5975974

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 8 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
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BASE COUNT 1 a 7 c 5 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgaccctc 17
|||||
Db 1 CCGCTGCGACCCCTC 14

RESULT 9
AR052612 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 10 from patent US 5831066.
DEFINITION AR052612
ACCESSION AR052612.1 GI:5975976
VERSION JP 2001503267-A/74.
KEYWORDS JP 2001503267-A/74.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed, J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 10 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
BASE COUNT 2 a 8 c 4 g 3 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgctgcgacc 14
|||||
Db 4 TACCGCTGCGACCC 17

RESULT 10
BD010808 24 bp DNA linear PAT 31-JAN-2002
LOCUS Novel polypeptide and DNA thereof.
DEFINITION BD010808
ACCESSION BD010808.1 GI:18639181
VERSION JP 2001069994-A/9.
KEYWORDS JP 2001069994-A/9.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 9 21-MAR-2001;
COMMENT TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001069994-A/9
PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911
PR YASUNAKI ITO, KAZUMORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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Location/Qualifiers
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Best Local Similarity 88.2%; Pred. No. 3.1e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 taccgctgcgaccctc 17
DB 2 TACCGCTGCGCCCATC 18

RESULT 11
AXI62807
LOCUS AXI62807 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6135 from Patent WO0140521.
ACCESSION AXI62807
VERSION AXI62807.1 GI:14544138
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6135 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
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Location/Qualifiers
misc-feature
/organism="Homo sapiens"
/db_xref="taxon:9606"
26
/note="1 of 2 allelic variants (6136 is other entry)
Accession number cg44914955"
BASE COUNT 13 a 21 c 11 g 6 t
ORIGIN

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Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgaccctc 17
DB 15 ACCGCTGCGACCCAC 30

RESULT 12
AXI62817
LOCUS AXI62817 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6145 from Patent WO0140521.
ACCESSION AXI62817

VERSION AXI62817.1 GI:14544148
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6145 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
1. 51
Location/Qualifiers
misc-feature
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/note="1 of 2 allelic variants (6146 is other entry)
Accession number cg44914955"
BASE COUNT 14 a 19 c 12 g 6 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgaccctc 17
DB 18 ACCGCTGCGACCCAC 33

RESULT 13
AXI62819
LOCUS AXI62819 51 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6147 from Patent WO0140521.
ACCESSION AXI62819
VERSION AXI62819.1 GI:14544150
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6147 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source
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Location/Qualifiers
misc-feature
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/db_xref="taxon:9606"
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/note="1 of 2 allelic variants (6148 is other entry)
Accession number cg44914955"
BASE COUNT 14 a 19 c 12 g 6 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 51;
Best Local Similarity 87.5%; Pred. No. 7.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgaccctc 17
DB 18 ACCGCTGCGACCCAC 33

RESULT 14
AXI62921
LOCUS AXI62921 18 bp DNA linear PAT 24-JUN-1998
DEFINITION Antisense oligonucleotide against WT1 mRNA.

ACCESSION E12921
VERSION E12921.1 GI:3251752
KEYWORDS JP 1997104629-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamagami, T., Inoue, K. and Sugiyama, H.
TITLE LEUKEMIA CELL PROLIFERATION INHIBITING AGENT CONTAINING ANTISENSE
JOURNAL OLIGONUCLEOTIDE DERIVATIVE AGAINST WILMS TUMOR GENE (WT1)
KISHIMOTO CHUZO, SUGIYAMA HARUO
COMMENT OS None
OC Artificial sequences.
PN JP 1997104629-A/1
PD 22-APR-1997
PF 16-MAY-1996 JP 1996144818
PR 01-JUN-1995 JP 95P 156672
PI YAMAGAMI TAMOTSU, INOUE KAZUJI, SUGIYAMA HARUO PC
A61K31/70, A61K48/00, C07H21/04;
CC strandedness: Single;
FH topology: Linear;
FH key Location/Qualifiers
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/db_xref="taxon:32644"
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ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 3.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accgcgtgcgacct 16
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DB 15 ACCGCATTCGACCT 1

RESULT 15
E21868 18 bp DNA linear PAT 07-FEB-2001
LOCUS E21868
DEFINITION Solid tumor remedy comprising expression inhibitor against Wilms
tumor (WT1).
ACCESSION E21868
VERSION E21868.1 GI:13023739
KEYWORDS JP 1999035484-A/1.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Haruo, S.
TITLE Solid tumor remedy comprising expression inhibitor against Wilms
tumor (WT1)
JOURNAL Patent: JP 1999035484-A 1 09-FEB-1999;
HARUO SUGIYAMA
COMMENT OS Unidentified
PN JP 1999035484-A/1
PD 09-FEB-1999
PF 16-JUL-1997 JP 1997191635
PR
PI HARUO SUGIYAMA
PC A61K45/00, A61K31/70, A61K38/00, A61K48/00
CC Strandedness: Single;
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Best Local Similarity 86.7%; Pred. No. 3.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accgcgtgcgacct 16
|||||
DB 4 ACCGCATTCGACCT 18

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Job time: 8357 sec

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.szlm75.rge

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21.133 Million cell updates/sec

Title: US-09-709-170A-9

Sequence: 1 taccgcgtgcgaccctc 17

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Post-processing: Minimum Match 0%

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	17	100.0	17	16	AA086651	Bcl-2 antisense O
2	17	100.0	18	19	AAV52546	Unmethylated CpG
3	17	100.0	18	19	AAV27720	Immunostimulatory
4	17	100.0	18	20	AAZ41906	IL-12 secretory i
5	17	100.0	18	21	AAZ47644	Parasitic infecti
6	17	100.0	18	21	AAZ47982	Immune remodeling
7	17	100.0	18	22	AAH50628	Natural killer ce
8	17	100.0	18	22	AAF98688	Immunostimulatory
9	17	100.0	18	22	AAF98931	Immunostimulatory

	10	15.4	90.6	20	22	AAH8722	Proto-oncogene bcl-2
	11	14	82.4	17	16	AAO86552	bcl-2 antisense ol
	12	14	82.4	17	16	AAO86650	bcl-2 antisense ol
	13	14	82.4	17	19	AAV28177	Antisense oligonuc
	14	14	82.4	17	19	AAV28173	Antisense oligonuc
	15	14	82.4	17	19	AAV28174	Antisense oligonuc
	16	14	82.4	17	20	AAV23684	Deletion sequence
	17	14	82.4	17	20	AAV23685	Deletion sequence
	18	14	82.4	17	20	AAV23686	Deletion sequence
	19	14	82.4	17	20	AAV18693	Target bcl-2 antis
	20	14	82.4	17	20	AAV18694	Target bcl-2 antis
	21	14	82.4	17	20	AAV18695	Target bcl-2 antis
	22	13.8	81.2	18	22	AAH27725	Control oligonucle
	23	13.8	81.2	24	22	AAV59071	MLP related PCR pr
	24	13	76.5	20	16	AAO86643	Antisense oligomer
	25	13	76.5	20	19	AAV28169	Antisense oligonuc
	26	13	76.5	20	20	AAV23681	Deletion sequence
	27	13	76.5	20	20	AAV18690	Target bcl-2 antis
	28	13	76.5	20	21	AAZ49348	bcl-2 targeted ant
	29	12.8	75.3	51	22	AAI79104	Human silent SNP c
	30	12.8	75.3	51	22	AAI79206	Human silent SNP c
	31	12.8	75.3	51	22	AAI79206	Human silent SNP c
	32	12.2	71.8	29	13	AAQ33869	Sequence upstream
	33	12.2	71.8	36	22	AAH46089	Synthetic primer 4
	34	12.2	71.8	54	14	AAQ47266	Lactate dehydrogen
	35	11.8	69.4	18	18	AAV45127	Oligo antisense to
	36	11.8	69.4	18	20	AAV15834	Nucleotide sequenc
	37	11.8	69.4	18	20	AAV15833	Nucleotide sequenc
	38	11.8	69.4	20	24	AB196304	Capture oligonucle
	39	11.8	69.4	24	24	AB189178	Capture oligonucle
	40	11.8	69.4	24	24	AB189179	Capture oligonucle
	41	11.8	69.4	45	14	AAQ38042	Oligonucleotide Bt
	42	11.8	69.4	51	22	AAI33119	Human SNP oligonuc
	43	11.8	69.4	54	14	AAQ47269	Lactate dehydrogen
	44	11.8	69.4	61	14	AAQ38043	Oligonucleotide Bt
	45	11.8	69.4	71	21	AAV29094	Human secreted pro

ALIGNMENTS

RESULT	1
AAQ86651	
ID	AAQ86651 standard; DNA; 17 BP

AC AAQ86651;

DT 27-SEP-1995 (first entry)

Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy
 KW Lymphoma; programmed cell death; ss.

OS Synthetic

FH	Key	Location/Qualifiers
1	1	1

```

/*tag= a
EM
EM

```

XX WO9508350-A
PN

30-MAP-1995

XX 20-SEP-1994. 94W0-11510725

AA 20-SEP-1993. 93TIS-012A256
PR

PA (REED/) REED J C

AA Reed JC;
PI

XX

DR WPI: 1995-139394/18.
 XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 XX
 PS Example 12; Page 33; 108bp; English.
 CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS11846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AA086650-55) or the 5'-cap
 CC region (AA086656-58) of human bcl-2 pre-mRNAs. The AA086651
 CC oligonucleotide provided pronounced DNA fragmentation.
 XX
 SO Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtgcgaccctc 17
 ||||||||||||||||
 DB 1 taccgcgtgcgaccctc 17

RESULT 2
 AAV2546
 ID AAV2546 standard; DNA; 18 BP.
 XX
 AC AAV2546;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Unmethylated CpG dinucleotide 1761.
 XX
 KM Unmethylated CpG dinucleotide; immune response; bacterial meningitis;
 KM natural killer cell activation; NK cell; Th2 response; neonatal sepsis;
 KM pulmonary disorder; asthma; environmentally induced airway disease;
 KM bacterial infection; endotoxaemia; therapy; cystic fibrosis;
 KM inflammatory bowel disease; ss.
 XX
 OS Synthetic.
 XX
 PN W09837919-A1.
 XX
 PD 03-SEP-1998.
 XX
 PF 25-FEB-1998; 98WO-US03678.
 XX
 PR 28-FEB-1997; 97US-0039405.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Krieg AM, Schwartz DA;
 XX
 DR WPI: 1998-480941/41.
 XX
 PT Use of nucleic acids containing an unmethylated CpG - for treating a
 PT subject having or at risk of having an acute decrement in air flow
 PT or inhibiting an inflammatory response
 XX
 PS Example 4; Page 35; 65pp; English.
 XX
 CC This sequence represents an unmethylated CpG dinucleotide, and can be
 CC used in the method of the invention. The method is for treating a subject
 CC having, or at risk of having an acute decrement in air flow, comprising
 CC administering a nucleic acid sequence containing at least one
 CC unmethylated CpG. The nucleic acids containing an unmethylated CpG
 CC dinucleotide affect an immune response in a subject by activating natural
 CC killer cells (NK) or redirecting a subject's immune response from a Th2
 CC to a Th1 response by inducing monocytic and other cells to produce Th1
 CC cytokines. They can be used to treat pulmonary disorders having an

CC immunologic component, such as asthma or environmentally induced airway
 CC disease. They can also be used to treat diseases associated with
 CC Gram-positive bacterial infections or endotoxaemia including bacterial
 CC meningitis, neonatal sepsis, cystic fibrosis, inflammatory bowel disease
 CC and liver cirrhosis, Gram-negative pneumonia, Gram-negative abdominal
 CC abscess, haemorrhagic shock, disseminated intravascular coagulation, or
 CC an inflammatory response to lipopolysaccharide.
 XX
 SO Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 18;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtgcgaccctc 17
 ||||||||||||||||
 DB 1 taccgcgtgcgaccctc 17

RESULT 3
 AAV27720
 ID AAV27720 standard; DNA; 18 BP.
 XX
 AC AAV27720;
 XX
 DT 01-OCT-1998 (first entry)
 XX
 DE Immunostimulatory oligodeoxyribonucleotide of the invention.
 XX
 KM Immunostimulatory; oligodeoxyribonucleotide; ODN;
 KM unmethylated CpG dinucleotide; activate; lymphocyte; immune response;
 KM Th2; cytokine; treatment; prevention; asthma; autoimmune disease;
 KM desensitisation therapy; artificial adjuvant; antibody generation; ss.
 XX
 OS Synthetic.
 XX
 PN W09818810-A1.
 XX
 PD 07-MAY-1998.
 XX
 PF 30-OCT-1997; 97WO-US19791.
 XX
 PR 30-OCT-1996; 96US-0738652.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Kline JN, Krieg AM;
 XX
 DR WPI: 1998-272127/24.
 XX
 PT New immunostimulatory nucleic acid molecules - which contain at
 PT least one unmethylated CpG dinucleotide, used for treating e.g.
 PT tumours, infections or autoimmune disease
 XX
 PS Disclosure; Page 49; 109pp; English.
 XX
 CC AAV27641-751 represent immunostimulatory oligodeoxyribonucleotides
 CC (ODNs) of the invention. The ODNs contain at least one unmethylated CpG
 CC dinucleotide, and have the formula:
 CC 5' N1X1CGX2N2 3', where at least one nucleotide separates consecutive
 CC CpGs, X1 is adenine, guanine, or thymine, X2 is cytosine or thymine, N
 CC is any nucleotide and N1+N2 is 0-26 bases with the provision that N1 and
 CC N2 does not contain a CCGG tetramer or more than one CCG or CCGG trimer
 CC OR 5' NX1X2CGX3X4N 3', where at least one nucleotide separates
 CC consecutive CpGs, X1 and X2 are selected from GPT, GPG, GGA, APT and APA,
 CC X3 and X4 are selected from TPT or CPT, N is any nucleotide and N1+N2 is
 CC 0-26 bases with the provision that N1 and N2 does not contain a CCGG
 CC tetramer or more than one CCG or CCGG trimer.
 CC The ODNs activate lymphocytes in a subject and redirect a subject's
 CC immune response from a Th2 to a Th1 (e.g. by inducing monocytic cells
 CC and other cells to produce Th1 cytokines, including IL-12, IFN-gamma and
 CC GM-CSF). The ODNs can be used to treat or prevent an asthmatic disorder,

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgcacctc 17
| | | | | | | | | | | | | | | | | | | |
Db 1 taccgcgtgcgcacctc 17

RESULT 6

AAZ47982
ID AAZ47982 standard; DNA: 18 BP.

AAZ47982;

08-MAR-2000 (first entry)

Immune remodeling inducing Cpg oligonucleotide SEQ ID NO:60.

Haematopoiesis; regulation; Cpg oligonucleotide; phosphorothioate;
immune remodeling; thrombopoiesis; anaemia; immune system; cancer;
immune response; allergic reaction; infectious disease; asthma;
thrombocytopenia; immunohaemolytic disorder; genetic disorder;
haemoglobinopathy; kidney failure; chronic inflammatory disorder;
rheumatoid arthritis; ss.

Synthetic.

WO958118-A2.

18-NOV-1999.

14-MAY-1999; 99WO-IB01285.

14-MAY-1998; 98US-0085516.

02-FEB-1999; 99US-0241653.

(CPG1-) CPG IMMUNOPHARMACEUTICALS GMBH.

(CPG1-) CPG IMMUNOPHARMACEUTICALS INC.

Wagner H, Lipford G;

Use of Cpg containing oligonucleotides for, e.g. inducing an
antigen-specific immune response

Example 1; Page 66; 116pp; English.

The present invention describes a method using Cpg containing
oligonucleotides (ONS) for regulating immune system remodeling and for
regulating haematopoiesis. The method for inducing an antigen-specific
immune response comprises: (1) administering an ON having a sequence
including at least the formula (1); and (2) exposing the subject to an
antigen at least 3 days after the ON is administered to the subject to
produce an antigen-specific immune response: 5' X1CGX2 3' (1), where
the ON = includes at least 8 nucleotides; C and G = unmethylated, and
X1 and X2 = nucleotides. The method can be used for inducing an immune
response against an antigen such as cells, cell extracts, proteins,
polysaccharides, polysaccharide conjugates, lipids, glycolipids,
carbohydrate, viral extracts, viruses, bacteria, fungi, parasites and
allergens. It can be used in a subject at risk of developing cancer or
an allergic reaction. It can also be used for treating an infectious
disease, allergic diseases and asthma, as well as thrombocytopenia
which is drug-induced, due to an autoimmune disorder such as idiopathic
thrombocytopenic purpura, or resulting from accidental or therapeutic
radiation exposure. It can also be used for treating anaemia such as
drug-induced anaemia, immunohaemolytic disorder, genetic disorders such
as haemoglobinopathy and inherited haemolytic anaemia, inadequate
production despite adequate iron stores, chronic disease such as kidney

failure, and chronic inflammatory disorder such as rheumatoid arthritis,
or anaemia resulting from accidental or therapeutic radiation exposure.
AAZ47932 to AAZ48029 represent phosphorothioate Cpg oligonucleotides
used in the exemplification of the present invention.

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgcacctc 17
| | | | | | | | | | | | | | | | | | | |
Db 1 taccgcgtgcgcacctc 17

RESULT 7

AAH50628
ID AAH50628 standard; DNA: 18 BP.

AAH50628;

22-AUG-2001 (first entry)

Natural killer cell lytic activity inducing oligonucleotide SEQ ID NO:60.

Immunostimulatory; inducing; natural killer cell; lytic activity;
unmethylated Cpg dinucleotide; immune response; B cell proliferation;
TNF; immune activation; interleukin 6; IL-6; interferon gamma;
IFN-gamma; cytokine; ss.

Homo sapiens.

Synthetic.

US6239116-B1.

29-MAY-2001.

30-OCT-1997; 97US-0960774.

30-OCT-1996; 96US-0738652.

(IOWA) UNIV IOWA RES FOUND.

(COLE-) COLEY PHARM GROUP INC.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Krieg AM, Kline JN;

WPI; 2001-380456/40.

Methods for inducing IL-6, interferon-gamma or IL-12, or stimulating
natural killer cell lytic activity in a human, comprise administering
to the subject or exposing a natural killer cell to immunostimulatory
nucleic acids

Disclosure; Column 32; 74pp; English.

The present invention describes methods for inducing interleukin 6
(IL-6), interferon-gamma (IFN-gamma) or IL-12, or for stimulating
natural killer cell lytic activity. The methods comprise administering
to the subject or exposing a natural killer cell to an immunostimulatory
nucleic acid. Also described are: (1) inducing IL-6 in a subject
comprising administering to the subject to induce IL-6 in the subject
the immunostimulatory nucleic acid; (2) stimulating natural killer cell
lytic activity comprising exposing a natural killer cell to the
immunostimulatory nucleic acid to stimulate natural killer cell lytic
activity; (3) inducing interferon-gamma in a subject to treat an immune
system deficiency comprising administering to the subject to induce
interferon-gamma production, the immunostimulatory nucleic acid; and
(4) inducing IL-12 in a subject comprising administering to the subject
the immunostimulatory nucleic acid. The methods are useful for inducing
IL-6, interferon-gamma or IL-12, or stimulating natural killer cell

lyric activity in a subject, particularly a human. The methods are particularly useful for modulating an immune response. AAH50571 to AAH50671 represent oligonucleotide sequences used in the exemplification of the present invention.

Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 taccgcgtgcgaccctc 17
|||||
DB 1 taccgcgtgcgaccctc 17

RESULT 8

AAf98888 standard; DNA; 18 BP.

AC AAF98888;

DT 12-JUN-2001 (first entry)

DE Immunostimulatory nucleic acid #4.

Vaccine: cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;

Immunostimulatory; tumour; viral infection; bacterial infection;
fungal infection; parasitic infection; cancer; asthma;
infectious disease; allergy; immune deficiency; phosphorothioate; ss.

Synthetic.

WO200122972-A2.

PD 05-APR-2001.

PF 25-SEP-2000; 2000WO-US26383.

PR 25-SEP-1999; 99US-0156113.

PR 27-SEP-1999; 99US-0156135.

PR 23-AUG-2000; 2000US-0227436.

PA (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

PI Krieg AM, Schetter C, Vollmer J;

WPI; 2001-273485/28.

Vaccinating against tumors, infectious diseases, allergies and asthma
using immunostimulatory Py-rich and Tg nucleic acids -

Disclosure; Page 38; 338pp; English.

The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or streptococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a T_H2 to a T_H1 immune response and to activate immune cells.

Note: the present sequence may have a phosphorothioate backbone.
Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 taccgcgtgcgaccctc 17
|||||
DB 1 taccgcgtgcgaccctc 17

RESULT 9

AAf98931 standard; DNA; 18 BP.

AC AAF98931;

DT 12-JUN-2001 (first entry)

DE Immunostimulatory nucleic acid #47.

Vaccine: cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;

Immunostimulatory; tumour; viral infection; bacterial infection;
fungal infection; parasitic infection; cancer; asthma;
infectious disease; allergy; immune deficiency; phosphorothioate; ss.

Synthetic.

WO200122972-A2.

PD 05-APR-2001.

PF 25-SEP-2000; 2000WO-US26383.

PR 25-SEP-1999; 99US-0156113.

PR 27-SEP-1999; 99US-0156135.

PR 23-AUG-2000; 2000US-0227436.

PA (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

PI Krieg AM, Schetter C, Vollmer J;

WPI; 2001-273485/28.

Vaccinating against tumors, infectious diseases, allergies and asthma
using immunostimulatory Py-rich and Tg nucleic acids -

Disclosure; Page 39; 338pp; English.

The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or streptococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a T_H2 to a T_H1 immune response and to activate immune cells.

Note: the present sequence may have a phosphorothioate backbone.
Sequence 18 BP; 2 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 22; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.3; 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 taccgcgtgcgaccctc 17
|||||

Db 1 taccgcgtcgaccctc 17

RESULT 10

ID AAH48722 standard: DNA; 20 BP.

XX AAH48722;

DT 19-OCT-2001 (first entry)

DE Proto-oncogene bcl-2 associated primer SEQ ID 3.

XX KW Primer; phosphorothioate; somatostatin; cytostatic; virucide; asthma;
XX antiinflammatory; antisthmatic; cardiant; antisense therapy;
XX cancer; viral disease; inflammatory process; somatostatin receptor;
XX central nervous system disease; cardiovascular disease; SSTR;
XX proto-oncogene; bcl-2; ss.

OS Unidentified.

XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= "OTHER"
FT /note= "phosphorothioate"

PN DE1006572-A1.

PD 23-AUG-2001.

PF 14-FEB-2000; 2000DE-1006572.

PR 14-FEB-2000; 2000DE-1006572.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

PI Eisenhut M, Mier W, Ertia R, Haberhorn U;

XX WPI: 2001-530596/59.

XX New conjugates of oligonucleotides with somatostatin analogs, useful in
PT antisense therapy, e.g. of viral, inflammatory or asthmatic disease or
PT especially tumors overexpressing the somatostatin receptor -

PS Example 3; Page 9; 16pp; German.

XX This invention describes a novel oligonucleotide conjugate (I) comprising
CC (a) an oligonucleotide, at least part of the sequence of which is
CC complementary to part of an intracellular nucleic acid sequence; and (b)
CC a somatostatin analog. The products of the invention have cytostatic,
CC virucide, antiinflammatory, antisthmatic and cardiant activity. The use
CC of (I) is claimed in antisense therapy, especially of cancer, viral
CC disease, inflammatory processes or asthmatic, central nervous system or
CC cardiovascular disease. (I) are especially used for therapy of tumors
CC overexpressing the somatostatin receptor (SSTR) (e.g. small-cell lung
CC tumors, breast tumors, brain tumors or other endocrine tumors), but are
CC also useful for treating viral diseases (e.g. herpes simplex-1
CC infection), inflammatory disease (typical target RNA the NF-kappa-B),
CC asthmatic disease (typical target RNA the adenosine A1 receptor), central
CC nervous system disease (typical target RNA the dopamine receptor) or
CC cardiovascular disease (typical target RNA c-myc). (I) are efficiently
CC taken up by cells and incorporated in target cells (via the SSTR) and are
CC highly selective for cells overexpressing SSTRs. This sequence
CC represents a primer used to illustrate the method of the invention.

XX Sequence 20 BP; 2 A; 7 C; 5 G; 6 T; 0 other;

Query Match 90.6%; Score 15.4; DB 22; Length 20;

Best Local Similarity 94.1%; Pred. No. 52;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 taccgcgtcgaccctc 17
DB 1 taccgcgtcgaccctc 17

RESULT 11

ID AA086652 standard: DNA; 17 BP.

XX AA086652;

DT 27-SEP-1995 (first entry)

DE bcl-2 antisense oligonucleotide.

XX KW Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX lymphoma; programmed cell death; ss.

OS Synthetic.

XX Key Location/Qualifiers
FH misc-feature 1..17
FT /*tag= a
FT /note= "3'-5' (antisense) sequence"

PN W09508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

XX (REED/) REED J C.

XX Reed JC;

XX WPI: 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108pp; English.

XX Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086650-55) or the 5'-cap
CC region (AA086656-58) of human bcl-2 pre-mRNAs. The AA086652
CC oligonucleotide provided pronounced DNA fragmentation.

SO Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtcgacc 14
DB 4 taccgcgtcgacc 17

RESULT 12

ID AA086650 standard: DNA; 17 BP.

XX AA086650;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW Lymphoma; programmed cell death; ss.
XX Synthetic.
XX OS
XX Key Location/Qualifiers
FH 1..17
FT misc-feature /*tag= a
FT /note= "3'-5' (antisense) sequence"
XX
XX WO9508350-A.
XX
XX 30-MAR-1995.
XX
XX 20-SEP-1994; 94WO-US10725.
XX
XX 20-SEP-1993; 93US-0124256.
XX
XX (REED/) REED J C.
XX
XX Reed JC;
XX
XX WPI: 1995-139394/18.
XX
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX Example 12; Page 33; 108pp; English.
XX
XX Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS1846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.
XX
XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;
SQ

Query Match 82.4%; Score 14; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgacccctc 17
|||||
Db 1 cgcgtgcgacccctc 14

RESULT 13
AAV28172
ID AAV28172 standard; DNA; 17 BP.
XX
XX AAV28172;
XX
XX 08-OCT-1998 (first entry)
XX
XX Antisense oligonucleotide to bcl-2 mRNA.
DE
XX Purification; oligonucleotide; matrix; affinity unit;
KW affinity purification; antisense; bcl-2; ss.
XX
XX Synthetic.
OS
XX WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
PI

XX
XX WPI: 1998-362922/31.
XX
XX Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX Disclosure; Page 79; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
XX Sequence 17 BP; 1 A; 7 C; 5 G; 4 T; 0 other;
SQ

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgacccctc 17
|||||
Db 1 cgcgtgcgacccctc 14

RESULT 14
AAV28173
ID AAV28173 standard; DNA; 17 BP.
XX
XX AAV28173;
XX
XX 08-OCT-1998 (first entry)
XX
XX Antisense oligonucleotide to bcl-2 mRNA.
DE
XX Purification; oligonucleotide; matrix; affinity unit;
KW affinity purification; antisense; bcl-2; ss.
XX
XX Synthetic.
OS
XX WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
PI
XX WPI: 1998-362922/31.
XX
XX Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX Disclosure; Page 79; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the

CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgacc 14
|||||
DB 4 taccgcgtgcgacc 17

RESULT 15

AAV28174
ID AAV28174 standard; DNA; 17 BP.

AC AAV28174;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

PF 18-DEC-1997; 97MO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 80; 183pp; English.

XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgacc 14
|||||
DB 4 taccgcgtgcgacc 17

Search completed: June 28, 2002, 22:40:13
Job time: 8089 sec

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.szlm75.rng

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:46 ; Search time 334.55 Seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-9

Perfect score: 17

Sequence: 1 tacccgctgcagccctc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents.NA: *
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCBUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES.

Result No.	Score	Query	Match	Length	DB	ID	Description
1	17	100.0	17	2	US-08-465-485A-9		Sequence 9, Appl
2	17	100.0	17	3	US-09-080-285-9		Sequence 28, Appl
3	17	100.0	18	4	US-09-030-701-28		Sequence 60, Appl
4	17	100.0	18	4	US-09-286-098-60		Sequence 60, Appl
5	17	100.0	18	4	US-08-960-774-60		Sequence 8, Appl
6	14	82.4	17	2	US-08-465-485A-8		Sequence 10, Appl
7	14	82.4	17	2	US-08-465-485A-10		Sequence 8, Appl
8	14	82.4	17	3	US-09-080-285-8		Sequence 10, Appl
9	14	82.4	17	3	US-09-080-285-10		Sequence 1, Appl
10	11.8	69.4	18	3	US-08-952-664-1		Sequence 2, Appl
11	11.8	69.4	18	4	US-09-487-874-1		Sequence 25, Appl
12	11.8	69.4	18	4	US-09-487-874-2		Sequence 25, Appl
13	11.8	69.4	31	1	US-08-095-726-25		Sequence 27, Appl
14	11.4	67.1	31	1	US-08-095-726-27		Sequence 22, Appl
15	11.4	67.1	31	1	US-08-096-043-22		Sequence 24, Appl
16	11.4	67.1	31	1	US-08-096-043-24		Sequence 18, Appl
17	11.4	67.1	31	1	US-08-093-577-18		Sequence 20, Appl
18	11.4	67.1	31	1	US-08-093-577-20		Sequence 30, Appl
19	11.4	67.1	31	1	US-08-096-623A-30		Sequence 32, Appl
20	11.4	67.1	31	1	US-08-096-623A-32		Sequence 97, Appl
21	11.4	67.1	19	4	US-09-038-637-97		Sequence 11, Appl
22	11.2	65.9	28	1	US-08-049-264C-11		Sequence 11, Appl
23	11.2	65.9	28	1	US-08-476-562-11		Sequence 11, Appl
24	11.2	65.9	28	1	US-08-479-723A-11		Sequence 11, Appl
25	11.2	65.9	28	5	PCR-US84-04310-11		Sequence 21, Appl
26	11.2	65.9	28	4	US-08-913-014A-21		
27	11.2	65.9	32	4			

28	11.2	65.9	44	1	US-08-282-030-12	Sequence 12, Appl
29	11.2	65.9	44	5	PCR-US95-10219-12	Sequence 12, Appl
30	11.2	65.9	54	4	US-09-082-649B-14	Sequence 14, Appl
31	11.2	65.9	55	3	US-08-928-881-17	Sequence 17, Appl
32	11.2	65.9	59	1	US-08-282-030-14	Sequence 14, Appl
33	11.2	65.9	59	5	PCR-US95-10219-14	Sequence 15, Appl
34	11.2	65.9	69	3	US-08-928-881-15	Sequence 53, Appl
35	11.2	65.9	70	4	US-09-037-990B-53	Sequence 11, Appl
36	11.1	64.7	17	2	US-08-465-485A-11	Sequence 11, Appl
37	11.1	64.7	17	3	US-09-080-285-11	Sequence 83, Appl
38	11.1	64.7	67	4	US-09-025-769B-83	Sequence 60, Appl
39	10.8	63.5	22	4	US-09-311-260-60	Sequence 56, Appl
40	10.8	63.5	26	1	US-08-049-264C-56	Sequence 56, Appl
41	10.8	63.5	26	1	US-08-476-562-56	Sequence 56, Appl
42	10.8	63.5	26	1	US-08-479-723A-56	Sequence 56, Appl
43	10.8	63.5	26	5	PCR-US94-04310-56	Sequence 5, Appl
44	10.8	63.5	30	1	US-08-106-761-5	
45	10.8	63.5	30	4	US-08-918-148-5	

ALIGNMENTS

RESULT 1
US-08-465-485A-9
; Sequence 9, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-9

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCAGCCCTC 17

RESULT 2

US-09-080-285-9
Sequence 9, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080.285
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCAGCCCTC 17

RESULT 3
US-09-030-701-28
Sequence 28, Application US/09030701B
Patent No. 6214806
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
TITLE OF INVENTION: UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
FILE REFERENCE: C1039/7011
CURRENT APPLICATION NUMBER: US/09/030,701B
PRIORITY FILING DATE: 1998-02-25
PRIORITY FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-28

Query Match 100.0%; Score 17; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 taccgcgtgcgaccctc 17

RESULT 4
US-09-286-098-60
Sequence 60, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286,098
PRIORITY FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic sequence
US-09-286-098-60

Query Match 100.0%; Score 17; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 taccgcgtgcgaccctc 17

RESULT 5

US-08-960-774-60
; Sequence 60, Application US/08960774
; Patent No. 6239116
; GENERAL INFORMATION:
; APPLICANT: Krieger et al.,
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,774
; FILING DATE: 30-October-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
; FILING DATE: October 30, 1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 08918/012001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-960-774-60

Query Match 100.0%; Score 17; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgaccctc 17
|||||
Db 1 TACCGCGTGCACCCCTC 17

RESULT 6
US-08-465-485A-8
; Sequence 8, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-8

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgaccctc 17
|||||
Db 1 CCGCGTGCACCCCTC 14

RESULT 7
US-08-465-485A-10
; Sequence 10, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-10

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgcgtgcgacc 14
|||||
DB 4 TACCGCGTGCAC 17

RESULT 8
US-09-080-285-8
Sequence 8, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
US-09-080-285-10

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-8

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 cgcgtgcgaccctc 17
|||||
DB 1 CGCGTGCACCTC 14

RESULT 9
US-09-080-285-10
Sequence 10, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OHION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-10

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgctgcgacc 14
|||||
DB 4 TACCGCTGCGACC 17

RESULT 10
US-08-952-664-1
; Sequence 1, Application US/08952664
; Patent No. 6034235

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Haruo
APPLICANT: YAMAGAMI, Tamotsu
TITLE OF INVENTION: INOUE, Kazushi
TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS
TITLE OF INVENTION: COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS
NUMBER OF SEQUENCES: 22
TITLE OF INVENTION: TUMOR GENE (WT1)
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,664
FILING DATE: 01-DEC-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01394
FILING DATE: 24-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-156672
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 053466/0223

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
US-08-952-664-1

Query Match 69.4%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgacct 16
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DB 4 ACCGCATTCGACCT 18

RESULT 11

US-08-952-664-2/c
; Sequence 2, Application US/08952664
; Patent No. 6034235

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Haruo
APPLICANT: YAMAGAMI, Tamotsu
APPLICANT: INOUE, Kazushi
TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS
TITLE OF INVENTION: COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS
NUMBER OF SEQUENCES: 22
TITLE OF INVENTION: TUMOR GENE (WT1)
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,664
FILING DATE: 01-DEC-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/01394
FILING DATE: 24-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-156672
FILING DATE: 01-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 053466/0223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5399
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
US-08-952-664-2

Query Match 69.4%; Score 11.8; DB 3; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgacct 16
|||||
DB 15 ACCGCATTCGACCT 1

RESULT 12
US-09-487-874-1

; Sequence 1, Application US/09487874
; Patent No. 6277832

GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Haruo
APPLICANT: YAMAGAMI, Tamotsu

APPLICANT: INOUE, Kazushi
TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS
TITLE OF INVENTION: COMPRISING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/487,874
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,664
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-156672
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 053466/0223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
US-09-487-874-1

Query Match 69.4%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgacct 16
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DB 4 ACCGCATTCGACCT 18

RESULT 13
US-09-487-874-2/c
Sequence 2, Application US/09487874
Patent No. 6277832
GENERAL INFORMATION:
APPLICANT: SUGIYAMA, Haruo
APPLICANT: YAMAGAMI, Tamotsu
APPLICANT: INOUE, Kazushi
TITLE OF INVENTION: GROWTH INHIBITOR FOR LEUKEMIA CELLS
TITLE OF INVENTION: COMPOSING ANTISENSE OLIGONUCLEOTIDE DERIVATIVE TO WILMS
TITLE OF INVENTION: TUMOR GENE (WT1)
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/487,874
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/952,664
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-156672
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wegner, Harold C.
REGISTRATION NUMBER: 25,258
REFERENCE/DOCKET NUMBER: 053466/0223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic DNA"
US-09-487-874-2

Query Match 69.4%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgcgtgcgacct 16
||||| |||||
DB 15 ACCGCATTCGACCT 1

RESULT 14
US-08-095-726-25
Sequence 25, Application US/08095726
Patent No. 5530188
GENERAL INFORMATION:
APPLICANT: Ausich, Rodney L
APPLICANT: Brinkhaus, Friedrich L
APPLICANT: Mukharji, Indrani
APPLICANT: Proffitt, John H
APPLICANT: Yarger, James G
APPLICANT: Yen, Hwei-Che B
TITLE OF INVENTION: Beta-Carotene Biosynthesis in
TITLE OF INVENTION: Genetically Engineered Hosts
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Amoco Corp., Patents and Licensing Dept
STREET: 200 E Randolph St
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60680-0703
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,726
FILING DATE: 21-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/785,566
FILING DATE: 30-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, NO. 5530188val B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3128567180

TELEFAX: 3128564972
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-095-726-25

Query Match 67.1%; Score 11.4; DB 1; Length 31;
 Best Local Similarity 92.3%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 cgcgtagcaccct 16
 ||| |||||
 Db 4 CGCATGCGACCT 16

RESULT 15
 US-08-095-726-27/c
 Sequence 27, Application US/08095726
 Patent No. 5530188
 GENERAL INFORMATION:
 APPLICANT: Ausich, Rodney L.
 APPLICANT: Brinkhaus, Friedhelm L.
 APPLICANT: Mukherji, Indrani
 APPLICANT: Proffitt, John H.
 APPLICANT: Yarger, James G.
 APPLICANT: Yen, Hui-Che B.
 TITLE OF INVENTION: Beta-Carotene Biosynthesis in
 NUMBER OF SEQUENCES: 79
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Amoco Corp., Patents and Licensing Dept
 STREET: 200 E Randolph St
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60680-0703
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/095,726
 FILING DATE: 21-JUL-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/785,566
 FILING DATE: 30-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Galloway, No. 5530188val B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 3128567180
 TELEFAX: 3128564972
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-095-726-27

Query Match 67.1%; Score 11.4; DB 1; Length 31;
 Best Local Similarity 92.3%; Pred. No. 1.5e+03;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 cgcgtagcaccct 16

Db 28 CGCATGCGACCT 16

Search completed: June 28, 2002, 22:16:47
 Job time: 8273 sec

Mon Jul 1 08:41:01 2002

us-09-709-170a-9.szlm75.rni

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:06 ; Search time 3762.88 seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170a-10

Perfect score: 17

Sequence: 1 tctaccgcgtcgcacc 17

Scoring table: IDENTITY_NUC

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBml: *
1: gb_da: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_da: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htgo_inv: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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2	14	82.4	17	6 <td>AR052611</td> <td>AR052611 Sequence</td>	AR052611	AR052611 Sequence
3	14	82.4	17	6 <td>AR052613</td> <td>AR052613 Sequence</td>	AR052613	AR052613 Sequence
4	14	82.4	18	6 <td>ARI46348</td> <td>ARI46348 Sequence</td>	ARI46348	ARI46348 Sequence
5	14	82.4	18	6 <td>ARI54731</td> <td>ARI54731 Sequence</td>	ARI54731	ARI54731 Sequence
6	14	82.4	18	6 <td>AXI03812</td> <td>AXI03812 Sequence</td>	AXI03812	AXI03812 Sequence
7	14	82.4	18	6 <td>AXI03864</td> <td>AXI03864 Sequence</td>	AXI03864	AXI03864 Sequence
8	14	82.4	18	6 <td>AX355457</td> <td>AX355457 Sequence</td>	AX355457	AX355457 Sequence
9	14	82.4	18	6 <td>BD009122</td> <td>BD009122 Sequence</td>	BD009122	BD009122 Sequence
10	13.4	78.8	24	6 <td>BD010808</td> <td>BD010808 Sequence</td>	BD010808	BD010808 Sequence
11	12.2	71.8	27	6 <td>AX049228</td> <td>AX049228 Sequence</td>	AX049228	AX049228 Sequence
12	12.2	71.8	27	6 <td>AX049833</td> <td>AX049833 Sequence</td>	AX049833	AX049833 Sequence
13	12.2	71.8	27	6 <td>AX050831</td> <td>AX050831 Sequence</td>	AX050831	AX050831 Sequence
14	12.2	71.8	30	6 <td>A12656</td> <td>A12656 Sequence</td>	A12656	A12656 Sequence
15	12.2	71.8	30	6 <td>ARI05729</td> <td>ARI05729 Sequence</td>	ARI05729	ARI05729 Sequence
16	12.2	71.8	30	6 <td>AXI64810</td> <td>AXI64810 Sequence</td>	AXI64810	AXI64810 Sequence
17	11.8	69.4	26	6 <td>AR003421</td> <td>AR003421 Sequence</td>	AR003421	AR003421 Sequence
18	11.8	69.4	26	6 <td>I21210</td> <td>I21210 Sequence</td>	I21210	I21210 Sequence
19	11.8	69.4	26	6 <td>I74477</td> <td>I74477 Sequence</td>	I74477	I74477 Sequence
20	11.8	69.4	28	6 <td>AR003376</td> <td>AR003376 Sequence</td>	AR003376	AR003376 Sequence
21	11.8	69.4	28	6 <td>I21165</td> <td>I21165 Sequence</td>	I21165	I21165 Sequence
22	11.8	69.4	28	6 <td>I74432</td> <td>I74432 Sequence</td>	I74432	I74432 Sequence
23	11.8	69.4	35	6 <td>AR003405</td> <td>AR003405 Sequence</td>	AR003405	AR003405 Sequence
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26	11.8	69.4	35	6 <td>I21195</td> <td>I21195 Sequence</td>	I21195	I21195 Sequence
27	11.8	69.4	35	6 <td>I74461</td> <td>I74461 Sequence</td>	I74461	I74461 Sequence
28	11.8	69.4	35	6 <td>I74462</td> <td>I74462 Sequence</td>	I74462	I74462 Sequence
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30	11.8	69.4	36	6 <td>AR003408</td> <td>AR003408 Sequence</td>	AR003408	AR003408 Sequence
31	11.8	69.4	36	6 <td>I21196</td> <td>I21196 Sequence</td>	I21196	I21196 Sequence
32	11.8	69.4	36	6 <td>I21197</td> <td>I21197 Sequence</td>	I21197	I21197 Sequence
33	11.8	69.4	36	6 <td>I74463</td> <td>I74463 Sequence</td>	I74463	I74463 Sequence
34	11.8	69.4	36	6 <td>I74464</td> <td>I74464 Sequence</td>	I74464	I74464 Sequence
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37	11.8	69.4	45	6 <td>I74430</td> <td>I74430 Sequence</td>	I74430	I74430 Sequence
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39	11.8	69.4	51	6 <td>I21167</td> <td>I21167 Sequence</td>	I21167	I21167 Sequence
40	11.8	69.4	51	6 <td>I74434</td> <td>I74434 Sequence</td>	I74434	I74434 Sequence
41	11.8	69.4	56	6 <td>AR003380</td> <td>AR003380 Sequence</td>	AR003380	AR003380 Sequence
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44	11.8	69.4	62	9 <td>AB010683</td> <td>AB010683 Homo sapi</td>	AB010683	AB010683 Homo sapi
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ALIGNMENTS

RESULT	1	17 bp	DNA	Linear	PAT 29-SEP-1999
LOCUS	AR052612				
DEFINITION	Sequence	10 from patent US 5831066.			
ACCESSION	AR052612				
VERSION	AR052612.1	GI:5975976			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Reed, J.C.				
TITLE	Regulation of bcl-2 gene expression				
JOURNAL	Patent: US 5831066-A 10-03-NOV-1998;				
FEATURES	Location/Qualifiers				
source	1..17				
BASE COUNT	2 a 8 c 4 g 3 t				
ORIGIN	/organism="unknown"				

Query Match 100.0%; Score 17; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TCTTACCGGTGCGACC 17

RESULT 2
AR052611 17 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 9 from patent US 5831066.
ACCESSION AR052611
VERSION AR052611.1 GI:5975975
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 9 03-NOV-1998;
FEATURES
source location/Qualifiers
1..17
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 3 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccggtgcgac 17
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Db 1 TACCGGTGCGACC 14

RESULT 3
AR052613 17 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 11 from patent US 5831066.
ACCESSION AR052613
VERSION AR052613.1 GI:5975977
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 11 03-NOV-1998;
FEATURES
source location/Qualifiers
1..17
/organism="unknown"

BASE COUNT 1 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcttaccggtgcg 14
|||||
Db 4 TCTTACCGGTGCG 17

RESULT 4
AR146348 18 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 60 from patent US 6218371.
ACCESSION AR146348
VERSION AR146348.1 GI:15109537

KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
JOURNAL Immunotherapeutic oligonucleotides and cytokines
FEATURES
source Patent: US 6218371-A 60 17-APR-2001;
location/Qualifiers
1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccggtgcgac 17
|||||
Db 1 TACCGGTGCGACC 14

RESULT 5
AR154731 18 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 60 from patent US 6239116.
ACCESSION AR154731
VERSION AR154731.1 GI:15122784
KEYWORDS
SOURCE
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 60 29-MAY-2001;
FEATURES
source location/Qualifiers
1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccggtgcgac 17
|||||
Db 1 TACCGGTGCGACC 14

RESULT 6
AX103812 18 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION Sequence 4 from Patent WO0122972.
ACCESSION AX103812
VERSION AX103812.1 GI:13920009
KEYWORDS
SOURCE
ORGANISM synthetic construct.
artificial sequence.

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 4 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GMDH (DE)
location/Qualifiers
1..18

FEATURES
source

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN /organism="synthetic construct"
/db_xref="taxon:32630"

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
Db 1 TACCGCGTGCAGCC 14

RESULT 7
LOCUS AX103864 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 56 from Patent WO0122972.
ACCESSION AX103864
VERSION AX103864.1 GI:13920061
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 56 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
GmbH (DE)

FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
Db 1 TACCGCGTGCAGCC 14

RESULT 8
LOCUS AX355457 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 485 from Patent WO0197843.
ACCESSION AX355457
VERSION AX355457.1 GI:18620125
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (sites)
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
JOURNAL cancer
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)

FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
Db 1 TACCGCGTGCAGCC 14

RESULT 9
LOCUS BD009122 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunostimulatory nucleic acid molecules.
ACCESSION BD009122
VERSION BD009122.1 GI:18637495
KEYWORDS JP 2001503267-A/74.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg,A.M. and Kline,J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: JP 2001503267-A 74 13-MAR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION
OS Artificial Sequence
PN JP 2001503267-A/74
PD 13-MAR-2001
PF 30-OCT-1997 JP 1998520784
PR 30-OCT-1996 US 08/738652
PI ARTHUR M KRIEG,JOEL N KLINE
PC C07H21/00,C07H21/02,C07H21/04,A61K31/175,A61K31/335,A61K31/47,
A61K31/70

FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgacc 17
Db 1 TACCGCGTGCAGCC 14

RESULT 10
LOCUS BD010808 24 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010808
VERSION BD010808.1 GI:18639181
KEYWORDS JP 2001069994-A/9.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ito,T., Nishi,K., Ogata,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 9 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001069994-A/9
PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YURO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC
FH Key 1.24 Location/Qualifiers
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source 1.24
Location/Qualifiers
1.24
/db_xref='taxon:32630'
BASE COUNT 5 a 10 c 5 g 4 t
ORIGIN

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Best Local Similarity 93.3%; Pred. No. 2.9e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 ctaccgcgtgcgacc 17
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Db 1 CTACCGCGTGCGCC 15

RESULT 11
AX049228 27 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 337 from Patent WO0069896.
ACCESSION AX049228
VERSION AX049228.1 GI:12226046
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lu, P.S.
TITLE Molecular interactions in hematopoietic cells
JOURNAL Patent: WO 0069896-A 337 23-NOV-2000;
Arbor Vita Corporation (US)
FEATURES
source 1.27
Location/Qualifiers
/organism='synthetic construct'
/db_xref='taxon:32630'
/note='primer'
BASE COUNT 6 a 11 c 6 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
|||||
Db 7 TCCTACTGCTGAGACC 23

RESULT 12
AX049833 27 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 337 from Patent WO0069898.
ACCESSION AX049833
VERSION AX049833.1 GI:12226261
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.

artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lu, P.S.
TITLE Molecular interactions in allergy cells
JOURNAL Patent: WO 0069898-A 337 23-NOV-2000;
Arbor Vita Corporation (US)
FEATURES
source 1.27
Location/Qualifiers
/organism='synthetic construct'
/db_xref='taxon:32630'
/note='primer'
BASE COUNT 6 a 11 c 6 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
|||||
Db 7 TCCTACTGCTGAGACC 23

RESULT 13
AX050831 27 bp DNA linear PAT 12-JAN-2001
LOCUS
DEFINITION Sequence 337 from Patent WO0069897.
ACCESSION AX050831
VERSION AX050831.1 GI:12226744
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lu, P.S.
TITLE Molecular interactions in t cells
JOURNAL Patent: WO 0069897-A 337 23-NOV-2000;
Arbor Vita Corporation (US)
FEATURES
source 1.27
Location/Qualifiers
/organism='synthetic construct'
/db_xref='taxon:32630'
/note='primer'
BASE COUNT 6 a 11 c 6 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.3e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 tctaccgcgtgcgacc 17
|||||
Db 7 TCCTACTGCTGAGACC 23

RESULT 14
A12656 30 bp DNA linear PAT 10-DEC-1993
LOCUS
DEFINITION Oligonucleotide from patent w08606635.
ACCESSION A12656
VERSION A12656.1 GI:491432
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 30)
AUTHORS
TITLE ORAL VACCINES
JOURNAL Patent: WO 8606635-A 1 20-NOV-1986;
FEATURES
source 1.30
Location/Qualifiers

/organism="synthetic construct"
 /db_xref="taxon:32630"
 BASE COUNT 4 a 11 c 10 g 5 t
 ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 30;
 Best Local Similarity 82.4%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 tctaccgcgtgagacc 17
 ||||| || |||||
 Db 10 TCCTACGCGCTTCGACC 26

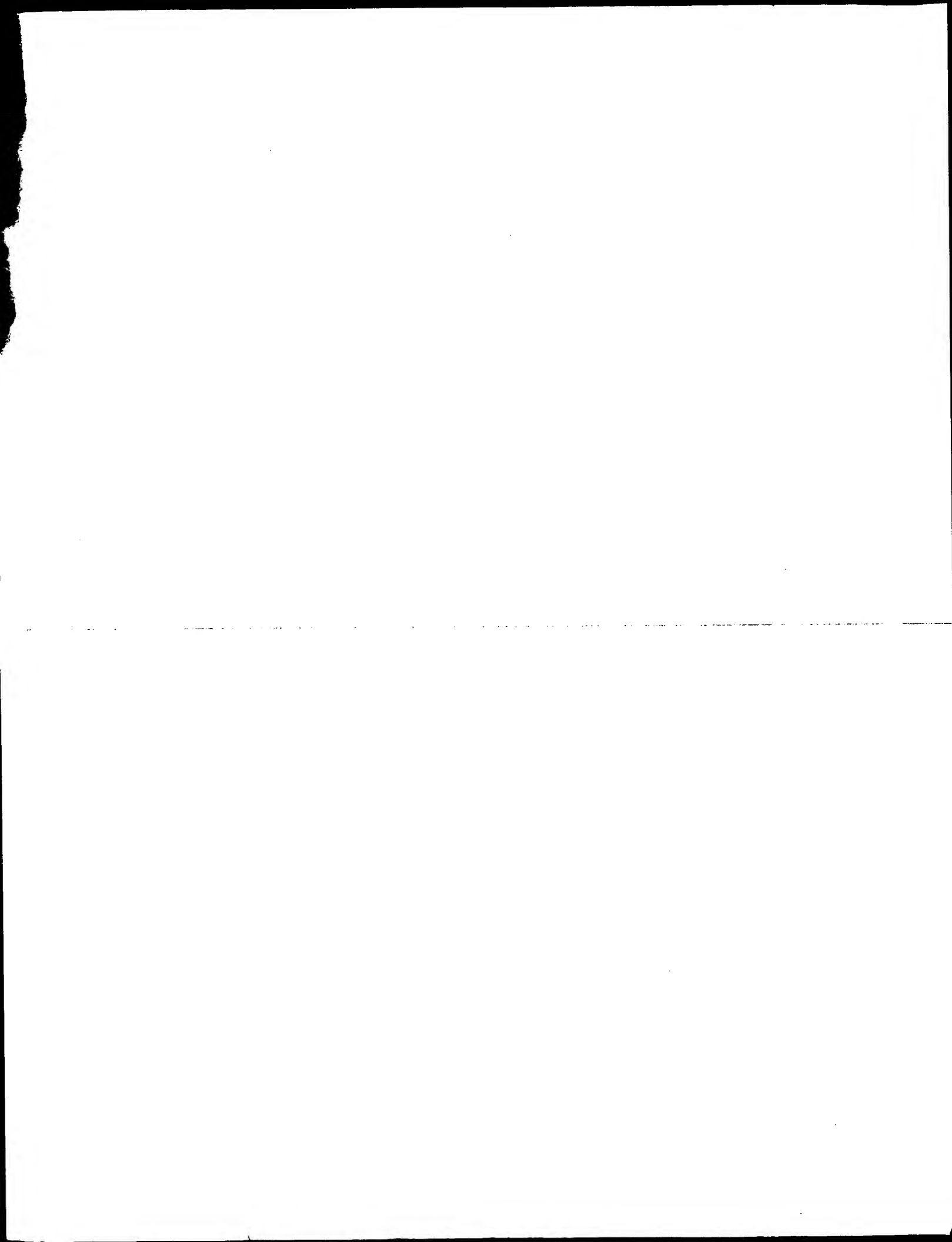
RESULT 15
 ARI05729
 LOCUS ARI05729 30 bp DNA linear PAT 14-FEB-2001
 DEFINITION Sequence 3 from patent US 6103243.
 ACCESSION ARI05729
 VERSION ARI05729.1 GI:12819794
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Russell-Jones, G. John, Howe, P., de Alzpuurua, H. James and
 Rand, K. Norman.
 TITLE Oral vaccines
 JOURNAL Patent: US 6103243-A 3 15-AUG-2000;
 FEATURES Location/Qualifiers
 source 1..30
 1..30

BASE COUNT 4 a 11 c 10 g 5 t
 ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 30;
 Best Local Similarity 82.4%; Pred. No. 1.2e+05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 tctaccgcgtgagacc 17
 ||||| || |||||
 Db 10 TCCTACGCGCTTCGACC 26

Search completed: June 28, 2002, 22:11:07
 Job time: 8358 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:13 ; Search time 1381.16 Seconds
(without alignments)
21.133 Million cell updates/sec

Title: US-09-709-170A-10

Perfect score: 17

Sequence: 1 tctaccgcgtgcgacc 17

Scoring table: IDENTITY-NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 1396432

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	AA086652	bcl-2 antisense ol
2	17	100.0	17	AAV28173	Antisense oligonuc
3	17	100.0	17	AAV28174	Antisense oligonuc
4	17	100.0	17	AAV23685	Deletion sequence
5	17	100.0	17	AAV23686	Target bcl-2 antis
6	17	100.0	17	AAV18694	Target bcl-2 antis
7	17	100.0	17	AAV18695	Antisense oligonuc
8	16	94.1	20	AA086643	Antisense oligonuc
9	16	94.1	20	AAV28169	Antisense oligonuc

10	16	94.1	20	AAV23681	Deletion sequence
11	16	94.1	20	AAV18690	Target bcl-2 antis
12	16	94.1	20	AAV49348	bcl-2 targeted an
13	14	82.4	17	AA086651	Bcl-2 antisense ol
14	14	82.4	17	AA086653	Bcl-2 antisense ol
15	14	82.4	17	AAV28175	Antisense oligonuc
16	14	82.4	17	AAV23687	Deletion sequence
17	14	82.4	17	AAV18696	Target bcl-2 antis
18	14	82.4	18	AAV18697	Antisense oligonuc
19	14	82.4	18	AAV27720	Immunostimulatory
20	14	82.4	18	AAV27720	IL-12 secretion in
21	14	82.4	18	AAV27720	Parasitic infectio
22	14	82.4	18	AAV27720	Immune remodeling
23	14	82.4	18	AAV27720	Natural killer cel
24	14	82.4	18	AAV27720	Immunostimulatory
25	14	82.4	18	AAV27720	Immunostimulatory
26	13.4	75.3	20	AAV59071	MLP related PCR pr
27	12.8	72.9	20	AAV59071	PCR primer used to
28	12.8	72.9	20	AAV59071	Proto-oncogene bcl
29	12.2	71.8	20	AAV59071	Primer #47 used to
30	12.2	71.8	20	AAV59071	Human tax interact
31	12.2	71.8	20	AAV59071	Human tax interact
32	12.2	71.8	20	AAV59071	Type XIII collagen
33	12.2	71.8	20	AAV59071	Human silent nonco
34	12.2	71.8	20	AAV59071	Human clone c92796
35	12.2	71.8	20	AAV59071	Human HMGI-C mRNA
36	12.2	71.8	20	AAV59071	Probe 1479 to Chla
37	12	70.6	19	AAV70263	Vector amplifying
38	11.8	69.4	26	AAV70263	Vector amplifying
39	11.8	69.4	26	AAV70263	Zipper adapter U-R
40	11.8	69.4	26	AAV70263	Gene specific zip
41	11.8	69.4	26	AAV70263	Human single nucle
42	11.8	69.4	31	AAV70263	Vector adapter cZR
43	11.8	69.4	35	AAV70263	Vector adapter ZR
44	11.8	69.4	35	AAV70263	Vector adapter pri
45	11.8	69.4	35	AAV70263	Vector adapter pri

ALIGNMENTS

RESULT 1	AA086652	standard; DNA: 17 BP.
ID	AA086652	
AC	AA086652	
XX		
AC	AA086652	
XX		
DT	27-SEP-1995	(first entry)
XX		
DE	Bcl-2 antisense oligonucleotide.	
XX		
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;	
KW	Lymphoma; programmed cell death; ss.	
XX		
OS	Synthetic.	
XX		
EH	Key	Location/Qualifiers
FT	misc-feature	1..17
FT		/*tag= a
FT		/note= "3'-5' (antisense) sequence"
XX		
PN	W09508350-A.	
XX		
PD	30-MAR-1995.	
XX		
PF	20-SEP-1994;	94WO-US10725.
XX		
PR	20-SEP-1993;	93US-0124256.
XX		
PA	(REED/) REED J C.	
XX		
PI	Reed JC;	
XX		

DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AA086550-55) or the 5'-cap
CC region (AA086556-58) of human bcl-2 pre-mRNAs. The AA086552
CC oligonucleotide provided pronounced DNA fragmentation.

XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
DB 1 tctaccgcgtgcgacc 17

RESULT 2

ID AAV28173 standard; DNA; 17 BP.

AC AAV28173;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

XX 25-JUN-1998.

PF 18-DEC-1997; 97MO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 79; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.

SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
DB 1 tctaccgcgtgcgacc 17

RESULT 3

ID AAV28174 standard; DNA; 17 BP.

AC AAV28174;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

XX 25-JUN-1998.

PF 18-DEC-1997; 97MO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

PS Disclosure; Page 80; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.

SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
DB 1 tctaccgcgtgcgacc 17

RESULT 4

AAV23685

ID	AXX23685	standard; DNA; 17 BP.
AC	AXX23685.	
XX		
DT	18-JUN-1999	(first entry)
XX		
DE	Deletion sequence oligonucleotide 138.	
XX		
OS	Synthetic.	
XX		
PN	WO9911820-A1.	
XX		
PD	11-MAR-1999.	
XX		
PF	01-SEP-1998;	98WO-US18084.
XX		
PR	02-SEP-1997;	97US-0923771.
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Chen D, Srivatsa GS;	
DR	WPI: 1999-205198/17.	
XX		
PT	New compositions comprising sensor arrays made up of unique probe	
PT	oligonucleotides - useful for characterizing a sample of target	
PT	deletion oligonucleotides	
XX		
PS	Example 9; Page 149; 163pp; English.	
XX		
CC	This invention describes a novel composition comprising a number of	
CC	sensor arrays, where each array comprises a unique probe	
CC	oligonucleotide, which is the reverse complement of part of a unique	
CC	target oligonucleotide present in a mixture of target deletion sequence	
CC	oligonucleotides. The compositions form a method for characterizing a	
CC	sample of target deletion oligonucleotides which are labelled and	
CC	hybridize with the probe oligonucleotides of the sensor arrays. Such	
CC	oligonucleotides and their targets are represented in AXX23548-X23709.	
CC	Oligonucleotides characterized by the method form pharmaceutical	
CC	compositions that are useful for modulating cellular adhesion or	
CC	proliferation, and being active against a eukaryotic pathogen, a human	
CC	retrovirus, a human immunodeficiency virus (HIV), or a non-human	
CC	retrovirus, including influenza virus, Epstein-Barr virus, Respiratory	
CC	syncytial virus or cytomegalovirus (CMV). The compositions enable	
CC	characterization of deletion sequence oligonucleotides having related,	
CC	but different nucleobase sequences, and quantification of different	
CC	species of deletion sequence ("target") oligonucleotides in a mixture.	
CC	Also, if the specificity of the oligonucleotide's nucleobase sequence	
CC	for its reverse complement is not modified, the method may be performed	
CC	using oligodeoxynucleotides.	
XX		
XX		
SO	Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;	
XX		
Query Match	100.0%;	Score 17; DB 20; Length 17;
Best Local Similarity	100.0%;	Pred. No. 5.9;
Matches 17; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 tctaccgcgtgcgacc 17	
DB	1 tctaccgcgtgcgacc 17	
XX		
RESULT	5	
AXX23686	AXX23686 standard; DNA; 17 BP.	
XX		
AC	AXX23686;	

	XX	18-JUN-1999	(first entry)
DT	XX		
DE	XX	Deletion sequence oligonucleotide 139.	
XX	XX		
KW	RN	Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;	
KM	probe; cellular adhesion modulator; cellular proliferation modulator;		
KH	human retrovirus; human immunodeficiency virus; non-human retrovirus;		
XK	HIV; primer; ss.		
OS	Synthetic.		
XX			
PV	WO9911820-A1.		
PD	11-MAR-1999.		
PF	01-SEP-1998; 98WO-US18084.		
PR	02-SEP-1997; 97US-0923771.		
PA	(ISIS-) ISIS PHARM INC.		
PI	Chen D, Srivatsa GS;		
DJ	WPt: 1999-205198/17.		
PT	New compositions comprising sensor arrays made up of unique probe		
PT	deletion oligonucleotides - useful for characterizing a sample of target		
PS	Example 9; Page 149; 163pp; English.		
XX			
CC	This invention describes a novel composition comprising a number of		
CC	sensory arrays, where each array comprises a unique probe		
CC	oligonucleotide, which is the reverse complement of part of a unique		
CC	target oligonucleotide present in a mixture of target deletion sequence		
CC	oligonucleotides. The compositions form a method for characterizing a		
CC	sample of target deletion oligonucleotides which are labelled and		
CC	hybridize with the probe oligonucleotides of the sensory arrays. Such		
CC	oligonucleotides and their targets are represented in AAX23548-X23709.		
CC	Oligonucleotides characterized by the method from pharmaceutical		
CC	compositions that are useful for modulating cellular adhesion or		
CC	proliferation, and being active against a eukaryotic pathogen, a human		
CC	retrovirus, a human immunodeficiency virus (HIV), or a non-human		
CC	retrovirus, including influenza virus, Epstein-Barr virus, Respiratory		
CC	syncytial virus or cytomegalovirus (CMV). The compositions enable		
CC	characterization of deletion sequence oligonucleotides having related,		
CC	but different nucleobase sequences, and quantification of different		
CC	species of deletion sequence ("target") oligonucleotides in a mixture.		
CC	Also, if the specificity of the oligonucleotide's nucleobase sequence		
CC	for its reverse complement is not modified, the method may be performed		
CC	using oligodeoxynucleotides.		
SQ	Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other:		
QY	Query Match 100.0%; Score 17; DB 20; Length 17; Best local Similarity 100.0%; Pred. No. 5.9; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
ID	1 tctaccgcgtgagcc 17 1 ttctacgccgtggcacc 17		
AAIX18694 standard; DNA: 17 BP.			
DT	10-MAY-1999 (first entry)		

XX 30-MAR-1995.
PD 20-SEP-1994; 94WO-US10725.
XX 20-SEP-1993; 93US-0124256.
XX (REED/) REED J C.
XX Reed JC;
XX WPI; 1995-139394/18.
DR Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX Disclosure: Page 13; 108pp; English.
PS
XX The antisense oligonucleotide T1-AS straddles the translation-
CC initiation site in the mRNA coding strand of the human bcl-2
CC gene and is complementary to this region. It reduces the
CC expression of bcl-2 gene product thereby inducing programmed cell
CC death of certain cancer cells.
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 94.1%; Score 16; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgac 16
| | | | | | | | | | | | | | | | | | | | | |
Db 5 tctaccgcgtgcgac 20

RESULT 9
AAV28169
ID AAV28169 standard; DNA; 20 BP.
XX
AC AAV28169;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
XX Purification; oligonucleotide; matrix; affinity unit;
KW affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PE 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
XX
XX WPI; 1998-362922/31.
DR
XX
XX Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX Disclosure: Page 76; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that

CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 94.1%; Score 16; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgac 16
| | | | | | | | | | | | | | | | | | | | | |
Db 5 tctaccgcgtgcgac 20

RESULT 10
AAV23681
ID AAV23681 standard; DNA; 20 BP.
XX
AC AAV23681;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 134.
XX
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PE 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX
XX WPI; 1999-205198/17.
DR
XX
XX New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 147; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable

CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.

XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 94.1%; Score 16; DB 20; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccgcgtgcgac 16
|||||
Db 5 tctaccgcgtgcgac 20

RESULT 11

AA18690
ID AA18690 standard; DNA: 20 BP.

XX AAX18690;

XX 10-MAY-1999 (first entry)

XX Target bcl-2 antisense oligonucleotide #22.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
XX alimentary canal; transport; gastrointestinal mucosa; cancer;
XX Alzheimer's disease; beta-thalassemia; malaria; viral infection;
XX HIV; inflammation; ss.

XX Synthetic.

XX MO9901579-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98MO-US13574.

XX 01-JUL-1997; 97US-0886829.

XX (ISIS-) ISIS PHARM INC.

XX Hardee G, Teng C;

XX WPI; 1999-106077/09.

XX Composition comprising nucleic acid and penetration enhancer - used
XX particularly for delivering therapeutic antisense oligonucleotides
XX across the gastrointestinal mucosa, provides high bioavailability
XX Example 2; Page 83; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a
XX nucleic acid and at least one penetration enhancer. The compositions are
XX used: (i) to treat or prevent any disease or disorder that can be
XX treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
XX beta-thalassemia, malaria, viral infections (including human immune
XX deficiency virus (HIV)), inflammation, in human or animal medicine;
XX (ii) to investigate the role of a gene or gene product in non-human
XX animals; and (iii) to modulate gene expression in cells, tissues or
XX organs. The compositions provide bioavailability of at least 15,
XX preferably 17-35%. The penetration enhancer improves: (i) transport of
XX the nucleic acid across the mucosa of the alimentary canal and into
XX cells; and (ii) increases stability of the nucleic acid. Oral
XX administration avoids the complications and expense of intravenous or
XX other methods of administration. AAX18690 to AAX18799 and AAX18801
XX represent antisense oligonucleotides which can be used as the nucleic
XX acid in the method of the invention.

XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 94.1%; Score 16; DB 20; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccgcgtgcgac 16
|||||
Db 5 tctaccgcgtgcgac 20

RESULT 12

AA249348
ID AA249348 standard; DNA: 20 BP.

XX AA249348;

XX 14-MAR-2000 (first entry)

XX bcl-2 targeted antisense oligonucleotide SEQ ID 13.

XX Cellular proliferation; expression; modulation; antisense;
XX non-parenteral; delivery; uptake; administration; emulsion;
XX ulcerative colitis; Crohn's disease; inflammatory bowel disease;
XX ss.

XX Synthetic.

XX Homo sapiens.

XX WO9960012-A1.

XX 25-NOV-1999.

XX 20-MAY-1999; 99MO-US11394.

XX 21-MAY-1998; 98US-0082624.

XX (ISIS-) ISIS PHARM INC.

XX Teng C, Cook PD, Tillman L, Hardee GE, Ecker DJ, Manoharan M;

XX WPI; 2000-072428/06.

XX New oligonucleotide compositions used for the non-parenteral delivery
XX of e.g. antisense oligos, ribozymes, peptide nucleic acids, molecular
XX decoys, external guide sequences or aptamers -
XX Example 2; Page 122; 133pp; English.

XX Sequences AA249344-249354, AA249384-249385, AA249387-249388 and
XX AA249392-249393 represent antisense oligonucleotides designed
XX to modulate the rate of cellular proliferation. The invention relates to
XX new compositions for the non-parenteral delivery of oligonucleotides
XX comprising at least one oligonucleotide in an emulsion. Oligonucleotides
XX delivered via the compositions of the invention can be used to modulate
XX expression of a cellular adhesion protein, modulate a rate of cellular
XX proliferation, or have biological activity against eukaryotic pathogens
XX or retroviruses. They can be used for treating conditions including
XX e.g., ulcerative colitis, Crohn's disease, inflammatory bowel disease
XX or undue cellular proliferation. The compositions can enhance the local
XX and systemic uptake and delivery of nucleic acids via non-parenteral
XX routes of administration (e.g., via the alimentary canal, skin, eyes,
XX pulmonary tract, urethra or vagina).

XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match

Best Local Similarity 94.1%; Score 16; DB 21; Length 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tctaccgcgtgcgac 16

Db 5 ttcctaccgctgcgac 20

RESULT 13

AAQ86651
ID AAQ86651 standard; DNA; 17 BP.

AC AAQ86651;

DT 27-SEP-1995 (first entry)

DE bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

OS Synthetic.

FT key Location/Qualifiers
FT misc_feature 1..17
FT /tag= a
FT /note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI: 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PS of human solid tumours, esp. breast cancer

Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RSI1846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs. The AAQ86651
CC oligonucleotide provided pronounced DNA fragmentation.

SO Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgctgcgac 17
|||||

DB 1 taccgctgcgac 14

RESULT 14

AAQ86653
ID AAQ86653 standard; DNA; 17 BP.

AC AAQ86653;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW Lymphoma; programmed cell death; ss.
OS Synthetic.

FT key Location/Qualifiers
FT misc_feature 1..17
FT /tag= a
FT /note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI: 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PS of human solid tumours, esp. breast cancer

Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RSI1846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.

SO Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttcctaccgctgcg 14
|||||

DB 4 ttcctaccgctgcg 17

RESULT 15

AAV28175
ID AAV28175 standard; DNA; 17 BP.

AC AAV28175;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI: 1998-362922/31.

XX Matrix for selective separation of oligo:nucleotide - useful for,
 PT e.g. large scale purification of anti-sense agents from their
 PT deletion derivatives formed during synthesis

XX PS Disclosure: Page 81, 183pp: English.

XX AAV28155-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridising portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.

XX SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;

Best Local Similarity 100.0%; Pred No. 2.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tcctaccgcgtgcg 14
 |||||
 DB 4 tcctaccgcgtgcg 17

Search completed: June 28, 2002, 22:40:13
 Job time: 8089 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:47 ; Search time 334.55 Seconds
(without alignments)
12,482 Million cell updates/sec

Title: US-09-709-170A-10

Perfect score: 17

Sequence: 1 tctaccgcgtgcgacc 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA: *
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	US-08-465-485A-10	Sequence 10, Appl
2	17	100.0	17	US-09-080-285-10	Sequence 10, Appl
3	17	100.0	17	US-08-465-485A-9	Sequence 9, Appl
4	14	82.4	17	US-08-465-485A-11	Sequence 11, Appl
5	14	82.4	17	US-09-080-285-9	Sequence 9, Appl
6	14	82.4	17	US-09-080-285-11	Sequence 11, Appl
7	14	82.4	18	US-09-030-701-28	Sequence 28, Appl
8	14	82.4	18	US-09-286-098-60	Sequence 60, Appl
9	14	82.4	18	US-08-960-774-60	Sequence 60, Appl
10	12.2	71.8	60	US-08-458-614-3	Sequence 3, Appl
11	12.2	71.8	60	US-08-897-527-3	Sequence 3, Appl
12	12.2	71.8	60	US-08-897-527-4	Sequence 4, Appl
13	12.2	71.8	60	US-09-072-508-3	Sequence 3, Appl
14	12.2	71.8	60	US-09-072-508-4	Sequence 4, Appl
15	12.2	71.8	66	US-08-185-949B-85	Sequence 85, Appl
16	12.2	71.8	75	US-08-897-527-2	Sequence 2, Appl
17	12.2	71.8	75	US-09-072-508-2	Sequence 2, Appl
18	11.8	69.4	26	US-08-049-264C-56	Sequence 56, Appl
19	11.8	69.4	26	US-08-476-562-56	Sequence 56, Appl
20	11.8	69.4	26	US-08-479-723A-56	Sequence 56, Appl
21	11.8	69.4	26	PCT-US94-04310-56	Sequence 56, Appl
22	11.8	69.4	28	US-08-049-264C-11	Sequence 11, Appl
23	11.8	69.4	28	US-08-476-562-11	Sequence 11, Appl
24	11.8	69.4	28	US-08-479-723A-11	Sequence 11, Appl
25	11.8	69.4	35	PCT-US94-04310-11	Sequence 11, Appl
26	11.8	69.4	35	US-08-049-264C-40	Sequence 40, Appl
27	11.8	69.4	35	US-08-049-264C-41	Sequence 41, Appl

ALIGNMENTS

28	11.8	69.4	35	1	US-08-476-562-40	Sequence 40, Appl
29	11.8	69.4	35	1	US-08-476-562-41	Sequence 41, Appl
30	11.8	69.4	35	1	US-08-479-723A-40	Sequence 40, Appl
31	11.8	69.4	35	1	US-08-479-723A-41	Sequence 41, Appl
32	11.8	69.4	35	5	PCT-US94-04310-40	Sequence 40, Appl
33	11.8	69.4	35	5	PCT-US94-04310-41	Sequence 41, Appl
34	11.8	69.4	36	1	US-08-049-264C-42	Sequence 42, Appl
35	11.8	69.4	36	1	US-08-049-264C-43	Sequence 43, Appl
36	11.8	69.4	36	1	US-08-476-562-42	Sequence 42, Appl
37	11.8	69.4	36	1	US-08-476-562-43	Sequence 43, Appl
38	11.8	69.4	36	1	US-08-479-723A-42	Sequence 42, Appl
39	11.8	69.4	36	1	US-08-479-723A-43	Sequence 43, Appl
40	11.8	69.4	36	5	PCT-US94-04310-42	Sequence 42, Appl
41	11.8	69.4	36	5	PCT-US94-04310-43	Sequence 43, Appl
42	11.8	69.4	45	1	US-08-049-264C-9	Sequence 9, Appl
43	11.8	69.4	45	1	US-08-476-562-9	Sequence 9, Appl
44	11.8	69.4	45	1	US-08-479-723A-9	Sequence 9, Appl
45	11.8	69.4	45	5	PCT-US94-04310-9	Sequence 9, Appl

RESULT 1
US-08-465-485A-10
Sequence 10, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-10

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgctgagacc 17
|||||
DB 1 TCCTACCGCTGCGACC 17

RESULT 2
US-09-080-285-10
; Sequence 10, Application US/09080285
; Patent No. 6040181

GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-09-080-285-10

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctaccgctgagacc 17
|||||
DB 1 TCCTACCGCTGCGACC 17

RESULT 3
US-08-465-485A-9
; Sequence 9, Application US/08465485A
; Patent No. 5831066
GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
US-08-465-485A-9

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgctgagacc 17
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DB 1 TACCGGCTGCGACC 14

RESULT 4
US-08-465-485A-11
; Sequence 11, Application US/08465485A
; Patent No. 5831066
GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

US-08-465-485A-11
; Sequence 11, Application US/08465485A
; Patent No. 5831066
GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-11

Query Match
Best Local Similarity 100.0%; Score 14; DB 2; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tcttaccgctgcg 14
DB 4 tcttaccgctgcg 17

RESULT 5
US-09-080-285-9
Sequence 9, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-9

Query Match
Best Local Similarity 100.0%; Score 14; DB 3; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgctgcgacc 17
DB 1 taccgctgcgacc 14

RESULT 6
US-09-080-285-11
Sequence 11, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-11

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taccgcgtgcgac 14
|||||
Db 4 TCCTACCGCTGCG 17

RESULT 7
US-09-030-701-28
Sequence 28, Application US/09030701B
Patent No. 6214806
GENERAL INFORMATION:
APPLICANT: Krieg, Arthur M.
APPLICANT: Schwartz, David A.
TITLE OF INVENTION: USE OF NUCLEIC ACIDS CONTAINING
UNMETHYLATED CPG DINUCLEOTIDE IN THE TREATMENT OF
TITLE OF INVENTION: LPS-ASSOCIATED DISORDERS
FILE REFERENCE: C1039/7011
CURRENT APPLICATION NUMBER: US/09/030,701B
CURRENT FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/039,405
PRIOR FILING DATE: 1997-02-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 28
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-09-030-701-28

Query Match 82.4%; Score 14; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgac 17
|||||
Db 1 taccgcgtgcgac 14

RESULT 8
US-09-286-098-60
Sequence 60, Application US/09286098
Patent No. 6218371
GENERAL INFORMATION:

APPLICANT: Krieg, Arthur M.
APPLICANT: Weiner, George
TITLE OF INVENTION: Methods and Products for Stimulating the
TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
FILE REFERENCE: C1039/7026/HCL
CURRENT APPLICATION NUMBER: US/09/286,098
CURRENT FILING DATE: 1999-04-02
EARLIER APPLICATION NUMBER: US 60/080,729
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-60

Query Match 82.4%; Score 14; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 taccgcgtgcgac 17
|||||
Db 1 taccgcgtgcgac 14

RESULT 9
US-08-960-774-60
Sequence 60, Application US/08960774
Patent No. 6239116
GENERAL INFORMATION:
APPLICANT: Krieg et al.,
TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID MOLECULES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,774
FILING DATE: 30-October-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial No. 6239116 08/738,652
FILING DATE: October 30, 1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 08918/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-960-774-60

Query Match 82.4%; Score 14; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 taccgcgtgcgacc 17
|||||
DB 1 TACCGCGTCGACC 14

RESULT 10

US-08-458-814-3
Sequence 3, Application US/08458814
Patent No. 6103243
GENERAL INFORMATION:
APPLICANT: RUSSELL-JONES, Gregory J
APPLICANT: DE AIZPURA, Henry J
APPLICANT: HOME, Peter
APPLICANT: RAND, Keith N
TITLE OF INVENTION: ORAL VACCINES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,814
FILING DATE: 02-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/327,822
FILING DATE: 18-OCT-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US086/00135
FILING DATE: 14-MAY-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH3104
FILING DATE: 25-OCT-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PH0566
FILING DATE: 15-MAY-1985
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 60042/155/BIAU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
US-08-458-814-3

Query Match 71.8%; Score 12.2; DB 3; Length 30;
Best Local Similarity 82.4%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 tctaccgcgtgcgacc 17

|||||
DB 10 TCTACGCGCTTCGACC 26

RESULT 11

US-08-897-527-3/c
Sequence 3, Application US/08897527
Patent No. 6013770
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
APPLICANT: Zhang, Yuzhi
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,527
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-4"
US-08-897-527-3

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02; 3; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcgacc 17
|||||
DB 36 TCTACGCGCTTCGACC 20

RESULT 12

US-08-897-527-4/c
Sequence 4, Application US/08897527
Patent No. 6013770
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
APPLICANT: Zhang, Yuzhi
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/897,527
FILING DATE:
CLASSIFICATION: 51A
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-5"
US-08-897-527-4

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcacc 17
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DB 36 TCCTACGGCCTGCGGCC 20

RESULT 13
US-09-072-508-3/c
Sequence 3, Application US/09072508
Patent No. 6045799
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,508
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-4"
US-09-072-508-3

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcacc 17
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DB 36 TCCTACGGCCTGCGGCC 20

RESULT 14
US-09-072-508-4/c
Sequence 4, Application US/09072508
Patent No. 6045799
GENERAL INFORMATION:
APPLICANT: Reeves, Jerry J.
APPLICANT: Bertrand, Kevin P.
TITLE OF INVENTION: CHIMERIC CONTRACEPTIVE VACCINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,508
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28985/33989
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide LHRH-5"

US-09-072-508-4

Query Match 71.8%; Score 12.2; DB 3; Length 60;
Best Local Similarity 82.4%; Pred. No. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 tctaccgcgtgcacc 17
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DB 36 TCCTACGGCCTGCGGCC 20

RESULT 15
US-08-185-949B-85
Sequence 85, Application US/08185949B


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; Patent No. 5874279
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; APPLICANT: Richard D. Macdonald
; TITLE OF INVENTION: Recombinant Infectious Bovine
; TITLE OF INVENTION: Rhinotracheitis Virus
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM 330 466 DX2
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,949B
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 278-0525
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 66 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-185-949B-85

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Query Match 71.8%; Score 12.2; DB 2; Length 66;
Best Local Similarity 82.4%; Pred. NO. 4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

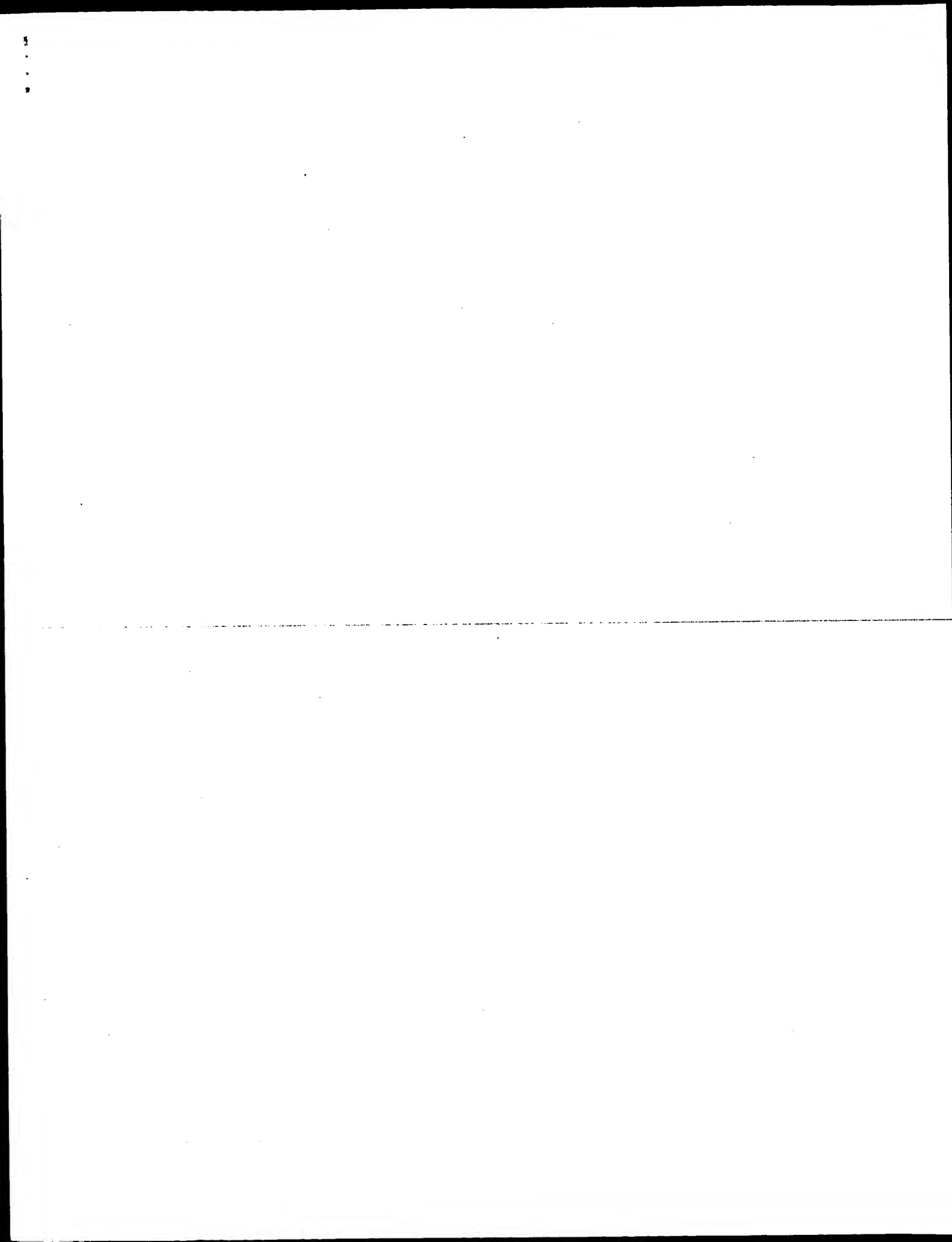
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Qy 1 tctaccgctgagacc 17
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Db 15 TCCTGCCGCGCGCGGCC 31

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Search completed: June 28, 2002, 22:16:47
Job time: 8273 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:07 ; Search time 3762.88 Seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170A-11

Perfect score: 17

Sequence: 1 cctctaccgcgctgcg 17

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
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8: gb.pl:*
9: gb.pr:*
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12: gb.sy:*
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14: gb.vi:*
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30: em.htg.hum:*
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32: em.htg.other:*
33: em.htg.in:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	12.8	75.3	68	6 <td>AX195437</td> <td>AX195437 Sequence</td>	AX195437	AX195437 Sequence
6	12.2	71.8	37	6 <td>AR121243</td> <td>AR121243 Sequence</td>	AR121243	AR121243 Sequence
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10	11.8	69.4	24	12 <td>AKM228027</td> <td>AKM228027 Artificial</td>	AKM228027	AKM228027 Artificial
11	11.8	69.4	24	6 <td>AR097966</td> <td>AR097966 Sequence</td>	AR097966	AR097966 Sequence
12	11.8	69.4	24	6 <td>AR16948</td> <td>AR16948 Sequence</td>	AR16948	AR16948 Sequence
13	11.8	69.4	26	6 <td>AR148920</td> <td>AR148920 Sequence</td>	AR148920	AR148920 Sequence
14	11.8	69.4	28	6 <td>AR148922</td> <td>AR148922 Sequence</td>	AR148922	AR148922 Sequence
15	11.8	69.4	28	6 <td>AR148927</td> <td>AR148927 Sequence</td>	AR148927	AR148927 Sequence
16	11.8	69.4	30	6 <td>AX003496</td> <td>AX003496 Sequence</td>	AX003496	AX003496 Sequence
17	11.8	69.4	48	6 <td>AX274545</td> <td>AX274545 Sequence</td>	AX274545	AX274545 Sequence
18	11.4	67.1	28	6 <td>AR122834</td> <td>AR122834 Sequence</td>	AR122834	AR122834 Sequence
19	11.4	67.1	28	6 <td>AR122835</td> <td>AR122835 Sequence</td>	AR122835	AR122835 Sequence
20	11.4	67.1	29	6 <td>AR122852</td> <td>AR122852 Sequence</td>	AR122852	AR122852 Sequence
21	11.4	67.1	29	6 <td>AR122853</td> <td>AR122853 Sequence</td>	AR122853	AR122853 Sequence
22	11.4	67.1	29	6 <td>AR122855</td> <td>AR122855 Sequence</td>	AR122855	AR122855 Sequence
23	11.4	67.1	29	6 <td>AR122857</td> <td>AR122857 Sequence</td>	AR122857	AR122857 Sequence
24	11.4	67.1	30	6 <td>AR122833</td> <td>AR122833 Sequence</td>	AR122833	AR122833 Sequence
25	11.4	67.1	51	6 <td>AX158311</td> <td>AX158311 Sequence</td>	AX158311	AX158311 Sequence
26	11.4	67.1	51	6 <td>AX158312</td> <td>AX158312 Sequence</td>	AX158312	AX158312 Sequence
27	11.4	67.1	51	6 <td>AX158313</td> <td>AX158313 Sequence</td>	AX158313	AX158313 Sequence
28	11.4	67.1	51	6 <td>AX158314</td> <td>AX158314 Sequence</td>	AX158314	AX158314 Sequence
29	11.4	67.1	61	6 <td>AR122795</td> <td>AR122795 Sequence</td>	AR122795	AR122795 Sequence
30	11.4	67.1	61	6 <td>AR122800</td> <td>AR122800 Sequence</td>	AR122800	AR122800 Sequence
31	11.4	67.1	74	9	S59798517	S59798517 PKLR-L-type
32	11.2	65.9	20	6 <td>AX191328</td> <td>AX191328 Sequence</td>	AX191328	AX191328 Sequence
33	11.2	65.9	22	6 <td>AR106739</td> <td>AR106739 Sequence</td>	AR106739	AR106739 Sequence
34	11.2	65.9	24	6 <td>AR149569</td> <td>AR149569 Sequence</td>	AR149569	AR149569 Sequence
35	11.2	65.9	24	6 <td>AX290693</td> <td>AX290693 Sequence</td>	AX290693	AX290693 Sequence
36	11.2	65.9	28	6 <td>AA0136</td> <td>AA0136 Sequence 12</td>	AA0136	AA0136 Sequence 12
37	11.2	65.9	28	6 <td>AR089991</td> <td>AR089991 Sequence</td>	AR089991	AR089991 Sequence
38	11.2	65.9	34	6 <td>AA0128</td> <td>AA0128 Sequence 4</td>	AA0128	AA0128 Sequence 4
39	11.2	65.9	45	6 <td>A17138</td> <td>A17138 Oligonucleo</td>	A17138	A17138 Oligonucleo
40	11.2	65.9	45	6 <td>AR027521</td> <td>AR027521 Sequence</td>	AR027521	AR027521 Sequence
41	11.2	65.9	60	6 <td>AR009386</td> <td>AR009386 Sequence</td>	AR009386	AR009386 Sequence
42	11.2	65.9	62	9 <td>AB010683</td> <td>AB010683 Homo sapi</td>	AB010683	AB010683 Homo sapi
43	11.2	65.9	74	9 <td>D86110</td> <td>D86110 Homo sapien</td>	D86110	D86110 Homo sapien
44	11	64.7	17	6 <td>AR052611</td> <td>AR052611 Sequence</td>	AR052611	AR052611 Sequence
45	11	64.7	17	6 <td>AR052615</td> <td>AR052615 Sequence</td>	AR052615	AR052615 Sequence

ALIGNMENTS

RESULT 1
AR052613 AR052613 17 bp DNA
LOCUS Sequence 11 from patent US 5831066.
DEFINITION AR052613
ACCESSION AR052613
VERSION AR052613.1 GI:5975977
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 11 03-NOV-1998;
FEATURES
source Location/Qualifiers
1..17
BASE COUNT 1 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 17; DB 6;
Best Local Similarity 100.0%; Pred. No. 3e+02; Length 17;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctg 17
Db 1 CCTTCTACCGGTCG 17

RESULT 2
LOCUS AR052612 17 bp DNA
DEFINITION Sequence 10 from patent US 5831066.
ACCESSION AR052612
VERSION AR052612.1 GI:5975976
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
JOURNAL Regulation of hcl-2 gene expression
FEATURES Patent: US 5831066-A 10 03-NOV-1998;
Location/Qualifiers
source 1..17
BASE COUNT 2 a 8 c 4 g 3 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctctaccgctg 17
Db 1 TCTTACCGGTCG 14

RESULT 3
LOCUS AR052614 17 bp DNA
DEFINITION Sequence 12 from patent US 5831066.
ACCESSION AR052614
VERSION AR052614.1 GI:5975978
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
JOURNAL Regulation of hcl-2 gene expression
FEATURES Patent: US 5831066-A 12 03-NOV-1998;
Location/Qualifiers
source 1..17
BASE COUNT 2 a 8 c 3 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctg 14
Db 4 CCTTCTACCGGTCG 17

RESULT 4
LOCUS S63038 52 bp DNA
DEFINITION T cell receptor V delta 1-J delta 1 junction (sample 127) [human,
adult, genomic, 52 nt].
ACCESSION S63038

VERSION S63038.1 GI:386400
KEYWORDS human adult.
SOURCE Homo sapiens
ORGANISM
REFERENCE 1 (bases 1 to 52)
AUTHORS Beldford,K., Beldford,C., MacIntyre,E., Even,P. and Sigaux,F.
TITLE Peripheral selection of V delta 1+ cells with restricted T cell
receptor delta gene junctional repertoire in the peripheral blood
of healthy donors
J. Exp. Med. 178 (1), 121-127 (1993)
JOURNAL 93301588
MEDLINE
REMARK Genbank staff at the National Library of Medicine created this
entry [NCBI gblbsg 134205] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
source 1..52
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene 1..52
/partial
BASE COUNT 10 a 17 c 11 g 14 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 9; Length 52;
Best Local Similarity 87.5%; Pred. No. 4.8e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cctctaccgctg 16
Db 20 CCTTCTACCGGTCG 35

RESULT 5
LOCUS AX195437 68 bp DNA
DEFINITION Sequence 36 from Patent WO0151646.
ACCESSION AX195437
VERSION AX195437.1 GI:15385983
KEYWORDS
SOURCE Aspergillus oryzae.
ORGANISM Aspergillus oryzae
REFERENCE 1 (bases 1 to 68)
AUTHORS Yaver,D.S. and Bellini,D.A.
TITLE Methods for producing a polypeptide using a crippled translational
initiator sequence
JOURNAL Patent: WO 0151646-A 36 19-JUL-2001;
Novozymes Biotech, Inc. (US)
FEATURES
source 1..68
Location/Qualifiers
/organism="Aspergillus oryzae"
/db_xref="taxon:5062"

BASE COUNT 16 a 13 c 24 g 15 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 68;
Best Local Similarity 87.5%; Pred. No. 4.5e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cctctaccgctg 17
Db 3 CTGCTACGGTCG 18

RESULT 6
LOCUS ARI21243 37 bp DNA
DEFINITION T cell receptor V delta 1-J delta 1 junction (sample 127) [human,
adult, genomic, 52 nt].
ACCESSION ARI21243

DEFINITION Sequence 23 from patent US 6159710.
ACCESSION AR121243
VERSION AR121243.1 GI:14104819
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 37)
AUTHORS Fraser,N.W., Zabolotny,J.M. and Krummenacher,C.F.
TITLE Method and compositions for stabilizing unstable gene transcripts
JOURNAL Patent: US 6159710-A 23 12-DEC-2000;
FEATURES
source Location/Qualifiers
BASE COUNT 5 a 18 c 10 g 4 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 37;
Best Local Similarity 82.4%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccttcaccgcgtgcg 17
||| ||| ||| ||| |||
Db 6 CCTCCTCCCGCGGCGC 22

RESULT 7
LOCUS AX159278 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 2606 from Patent WO0140521.
ACCESSION AX159278
VERSION AX159278.1 GI:14540609
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2606 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc-feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg4106315"
misc-feature 26
/note="2 of 2 allelic variants (2605 is other entry)"
BASE COUNT 6 a 21 c 12 g 11 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 50;
Best Local Similarity 82.4%; Pred. No. 1.1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccttcaccgcgtgcg 17
||| ||| ||| ||| |||
Db 13 CCTCCTCCCGCGGCGC 29

RESULT 8
LOCUS HSA132122 51 bp mRNA linear PRI 06-MAR-2000
DEFINITION Homo sapiens mRNA for T-cell receptor delta chain, CDR3 region
clone D28.
ACCESSION AJ132122
VERSION AJ132122.1 GI:4151017

KEYWORDS T-cell receptor delta; TCR delta chain.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Jouen-Beades,F., Halar,F., Drouot,L., Peyrat,M.A., Paris,E.,
Joly,P., Gilbert,D., Bonneville,M. and Tiron,F.
TITLE Expansion of circulating V gamma 9/V delta 1 T cells in a patient
with a syndrome of recurrent fever: evidence for an unusual
antigen-driven process leading to selection of recurrent motifs
within TCR junctional loops of diverse lengths
JOURNAL Eur.J Immunol. 29 (10), 3338-3349 (1999)
MEDLINE 20010072
REFERENCE 2 (bases 1 to 51)
AUTHORS Jouen-Beades,F.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1999) Jouen-Beades F., Immunologie, INSERM U519,
Faculte de Medecine, 22 boulevard Gambetta, 76183 Rouen cedex,
FRANCE
FEATURES
source Location/Qualifiers
1..51
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="D28"
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/product="T-cell receptor delta chain, CDR3 region"
/protein_id="CAI10585.1"
/db_xref="GI:4151018"
/translation="LGERRAFLRGGRADK"
BASE COUNT 11 a 10 c 21 g 9 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 9; Length 51;
Best Local Similarity 82.4%; Pred. No. 1e+05;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ccttcaccgcgtgcg 17
||| ||| ||| ||| |||
Db 17 CCTCCTCCCGCGGCGC 33

RESULT 9
LOCUS BD010808 24 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010808
VERSION BD010808.1 GI:18639181
KEYWORDS JP 2001069994-A/9.
SOURCE Synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 9 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Artificial Sequence
PN JP 2001069994-A/9
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N5/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//

PC C12P21/08.C12N15/00.A61K37/02.C12N5/00
CC
FH Key Location/Qualifiers
FT source 1..24
FT /organism='Artificial Sequence',
Location/Qualifiers
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source 1..24
/organism='synthetic construct'
/db_xref='taxon:32630'
BASE COUNT 5 a 10 c 5 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ctaccgcgtgq 17
|||||
DB 1 CTACCGCGTGG 12

RESULT 10
AMM229027/c 18 bp DNA linear SYN 09-NOV-1998
LOCUS Artificial Apis mellifera mellifera microsatellite PCR primer
DEFINITION
AP19-2.
ACCESSION AJ229027
VERSION AJ229027.1 GI:3858924
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequence.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baudry,E., Solignac,M., Garnery,L., Gries,M., Cornuet,J.M. and Koeniger,N.
TITLE Relatedness among honey bees of a drone congregation and its sociobiological consequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 18)
AUTHORS Solignac,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-1998) Solignac M., Laboratoire PGE, CNRS, Avenue de la Terrasse, 91198 Gif-sur-Yvette cedex, FRANCE
FEATURES
source 1..18
/organism='synthetic construct'
/db_xref='taxon:32630'
primer_bind 1..18
/note='PCR primer used to amplify Apis mellifera ssp. mellifera microsatellite locus Ap19'
/PCR_conditions='annealing temperature: 56 degC, MgCl2 concentration: 1.2 mM, length fragment 136 bp.'
BASE COUNT 6 a 3 c 2 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 12; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cttctaccgcgtgc 16
|||||
DB 17 CTTCCTACCGCGTAC 3

RESULT 11
AR097986 24 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 1 from patent US 6074823.
ACCESSION AR097986
VERSION AR097986.1 GI:12807243
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Koster,H.
TITLE DNA sequencing by mass spectrometry via exonuclease degradation
JOURNAL Patent: US 6074823-A 1 13-JUN-2000;
Location/Qualifiers
FEATURES
source 1..24
/organism='unknown'
BASE COUNT 6 a 9 c 4 g 5 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccttctaccgcgtg 15
|||||
DB 3 CATTCACCGCGTGG 17

RESULT 12
AR116948 24 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 1 from patent US 6140053.
ACCESSION AR116948
VERSION AR116948.1 GI:14097854
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Koster,H.
TITLE DNA sequencing by mass spectrometry via exonuclease degradation
JOURNAL Patent: US 6140053-A 1 31-OCT-2000;
Location/Qualifiers
FEATURES
source 1..24
/organism='unknown'
BASE COUNT 6 a 9 c 4 g 5 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccttctaccgcgtg 15
|||||
DB 3 CATTCACCGCGTGG 17

RESULT 13
AR148920/c 26 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 19 from patent US 6225531.
ACCESSION AR148920
VERSION AR148920.1 GI:15113010
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kakitani,M., Umemoto,N., Ishida,I., Iwamatsu,A., Yoshikawa,M. and Yamaoka,N.
TITLE Glucan elicitor receptor, DNA molecule coding therefor, and fungus-resistant plants transformed with the DNA molecule and method for creating the plants
JOURNAL Patent: US 6225531-A 19 01-MAY-2001;
Location/Qualifiers
FEATURES
source 1..26
/organism='unknown'

BASE COUNT 7 a 5 c 10 g 4 t
ORIGIN

Query Match

Best Local Similarity 69.4%; Score 11.8; DB 6; Length 26;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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|||||||
Db 26 CTCTCTACCCCATGC 12

RESULT 14

ARI48922 ARI48922 28 bp DNA Linear PAT 08-AUG-2001
LOCUS DEFINITION Sequence 21 from patent US 6225531.

ACCESSION ARI48922
VERSION ARI48922.1 GI:15113012

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Kakitani, M., Umemoto, N., Ishida, I., Iwamatsu, A., Yoshikawa, M. and Yamaoka, N.

TITLE Glucan elicitor receptor, DNA molecule coding therefor, fungus-resistant plants transformed with the DNA molecule and method for creating the plants
JOURNAL Patent: US 6225531-A 21 01-MAY-2001;

FEATURES Location/Qualifiers
1..28

BASE COUNT 5 a 10 c 5 g 8 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 28;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ctctctaccggtgc 16
|||||||
Db 11 CTCTCTACCCCATGC 25

RESULT 15

ARI48927 ARI48927 28 bp DNA Linear PAT 08-AUG-2001
LOCUS DEFINITION Sequence 26 from patent US 6225531.

ACCESSION ARI48927
VERSION ARI48927.1 GI:15113017

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 28)
AUTHORS Kakitani, M., Umemoto, N., Ishida, I., Iwamatsu, A., Yoshikawa, M. and Yamaoka, N.

TITLE Glucan elicitor receptor, DNA molecule coding therefor, fungus-resistant plants transformed with the DNA molecule and method for creating the plants
JOURNAL Patent: US 6225531-A 26 01-MAY-2001;

FEATURES Location/Qualifiers
1..28

BASE COUNT 5 a 10 c 5 g 8 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 28;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 11 CTCTCTACCCCATGC 25

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Job time: 8360 sec

Mon Jul 1 08:40:45 2002

us-09-709-170a-11.szlm75.rge

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-709-170A-11

Perfect score: 17

Sequence: 1 cctcctaccgcgtgcg 17

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Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	AA086653	Bcl-2 antisense ol
2	17	100.0	17	AAV28175	Antisense oligonuc
3	17	100.0	17	AAV23687	Deletion sequence
4	17	100.0	17	AAV18696	Target bcl-2 antls
5	17	100.0	20	AAQ86643	Antisense oligomer
6	17	100.0	20	AAV28169	Antisense oligonuc
7	17	100.0	20	AAV23681	Deletion sequence
8	17	100.0	20	AAV18690	Target bcl-2 antls
9	17	100.0	20	AA249348	bcl-2 targeted an

10	14	82.4	17	16	AA086652	Bcl-2 antisense ol
11	14	82.4	17	16	AA086654	Bcl-2 antisense ol
12	14	82.4	17	19	AAV28173	Antisense oligonuc
13	14	82.4	17	19	AAV28174	Antisense oligonuc
14	14	82.4	17	19	AAV28176	Antisense oligonuc
15	14	82.4	17	20	AAV23688	Deletion sequence
16	14	82.4	17	20	AAV23685	Deletion sequence
17	14	82.4	17	20	AAV23686	Deletion sequence
18	14	82.4	17	20	AAV18694	Target bcl-2 antls
19	14	82.4	17	20	AAV18695	Target bcl-2 antls
20	14	82.4	17	20	AAV18697	Target bcl-2 antls
21	13	76.5	19	17	AAV27370	Anti-ras oncogene
22	12.8	75.3	68	22	AAV08593	Aspergillus niger
23	12.2	71.8	24	19	AAV62489	Op 1e2 gene pa sig
24	12.2	71.8	25	19	AAV62494	Op 1e2 gene pa sig
25	12.2	71.8	28	18	AAV06292	Type XIII collagen
26	12.2	71.8	37	19	AAV64925	HSV-1 primer PEPB8
27	12.2	71.8	45	15	AAV06687	Purine rich region
28	12.2	71.8	50	22	AAV75665	Human silent SNP c
29	12.2	71.8	54	19	AAV64900	HSV-1 latency asso
30	12	70.6	19	19	AAV70263	Human HMGI-C mRNA
31	12	70.6	24	22	AAV59071	MVP related PCR pr
32	12	70.6	33	12	AAQ10110	Probe 1479 to Chla
33	11.8	69.4	17	21	AAV06292	Hammerhead ribozym
34	11.8	69.4	20	20	AAV95174	PCR primer used to
35	11.8	69.4	21	19	AAV25856	Human polymorphic
36	11.8	69.4	26	17	AAV09997	Primer for amplifi
37	11.8	69.4	26	18	AAV74651	Nucleotide sequenc
38	11.8	69.4	26	17	AAV29167	Primer for amplifi
39	11.8	69.4	28	17	AAV09999	Primer for amplifi
40	11.8	69.4	28	17	AAV10844	PCR primer U39 SEQ
41	11.8	69.4	28	18	AAV74653	Probe used to isol
42	11.8	69.4	30	20	AAV18662	Primer Y152R. Sy
43	11.8	69.4	32	20	AAV90786	permutin linker e
44	11.8	69.4	36	21	AAV5739	Human SNP oligonuc
45	11.8	69.4	50	22	AAV28176	

ALIGNMENTS

RESULT 1	
AA086653	AA086653 standard; DNA; 17 BP.
ID	
XX	AA086653;
AC	27-SEP-1995 (first entry)
XX	
DT	Bcl-2 antisense oligonucleotide.
XX	
DE	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
XX	Lymphoma; programmed cell death; ss.
KW	Synthetic.
XX	
OS	
XX	
PH	Key
FT	misc-feature
FT	Location/Qualifiers
FT	1.17
FT	/*tag= a
FT	/note= "3'-5' (antisense) sequence"
XX	
XX	WO9508350-A.
XX	
XX	30-MAR-1995.
XX	
XX	20-SEP-1994; 94WO-US10725.
XX	
XX	20-SEP-1993; 93US-0124256.
XX	
XX	(REED/) REED J C.
XX	
XX	Reed JC;
XX	

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
PS Example 12; Page 33; 108pp; English.
XX
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgcgctgcg 17
Db 1 cctctaccgcgctgcg 17

RESULT 2
AAV28175
ID AAV28175 standard; DNA; 17 BP.
XX
AC AAV28175;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
KW Purification; oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
XX
PT WPI; 1998-362922/31.
XX
DR Matrix for selective separation of oligonucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
PS Disclosure; Page 81; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridizing portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgcgctgcg 17
Db 1 cctctaccgcgctgcg 17

RESULT 3
AAV23687
ID AAV23687 standard; DNA; 17 BP.
XX
AC AAV23687;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 140.
XX
KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
PT WPI; 1999-205198/17.
XX
DR New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides
XX
PS Example 9; Page 150; 163pp; English.
XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labeled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23548-X23709.
CC oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including Influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

XX MO9827425-A1.
XX 25-JUN-1998.
XX 18-DEC-1997; 97WO-US23284.
XX 19-DEC-1996; 96US-0769951.
XX (ISIS-) ISIS PHARM INC.
XX Chen D, Cole DL, Srivatsa GS;
XX WPI, 1998-362922/31.
XX Matrix for selective separation of oligo:nucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX Disclosure; Page 76; 183pp; English.
XX AAV28155-268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridizing portion of the
XX target oligonucleotide. The matrix is used for affinity purification of
XX synthetic oligonucleotides, specifically antisense agents, for treatment
XX of hyperproliferative diseases, for treating a non-pathogen,
XX non-hyperproliferative disease, e.g. Alzheimer's, for modulating
XX expression of cell surface proteins, and to inhibit a eukaryotic
XX pathogen, retrovirus or other viruses.
XX Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 17; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 cctctaccgcgctgcg 17
Db 2 cctctaccgcgctgcg 18
RESULT 7
AA23681
ID AAX23681 standard; DNA: 20 BP.
XX AAX23681;
XX 18-JUN-1999 (first entry)
XX Deletion sequence oligonucleotide 134.
XX Deletion sequence oligonucleotide 134.
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; ss.
XX Synthetic.
XX WO9911820-A1.
XX 11-MAR-1999.
XX 01-SEP-1998; 98WO-US18084.
XX 02-SEP-1997; 97US-0923771.
XX (ISIS-) ISIS PHARM INC.
XX Chen D, Srivatsa GS;
PI

XX WPI, 1999-205198/17.
XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides
XX Example 9; Page 147; 163pp; English.
XX This invention describes a novel composition comprising a number of
XX sensor arrays, where each array comprises a unique probe
XX oligonucleotide, which is the reverse complement of part of a unique
XX target oligonucleotide present in a mixture of target deletion sequence
XX oligonucleotides. The compositions form a method for characterizing a
XX sample of target deletion oligonucleotides which are labeled and
XX hybridize with the probe oligonucleotides of the sensor arrays. Such
XX oligonucleotides and their targets are represented in AAX23548-X23709.
XX Oligonucleotides characterized by the method form pharmaceutical
XX compositions that are useful for modulating cellular adhesion or
XX proliferation, and being active against a eukaryotic pathogen, a human
XX retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX retrovirus, including Influenza virus, Epstein-Barr virus, Respiratory
XX Syncytial Virus or cytomegalovirus (CMV). The compositions enable
XX characterization of deletion sequence oligonucleotides having related,
XX but different nucleobase sequences, and quantification of different
XX species of deletion sequence ("target") oligonucleotides in a mixture.
XX Also, if the specificity of the oligonucleotide's nucleobase sequence
XX for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.
SQ
Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;
QY 1 cctctaccgcgctgcg 17
Db 2 cctctaccgcgctgcg 18
RESULT 8
AAX18690
ID AAX18690 standard; DNA: 20 BP.
XX AAX18690;
XX 10-MAY-1999 (first entry)
XX Target bcl-2 antisense oligonucleotide #22.
XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
XX alimentary canal; transport; gastrointestinal mucosa; cancer;
XX Alzheimer's disease; beta-thalassemia; malaria; viral infection;
XX HIV; inflammation; ss.
XX Synthetic.
XX WO9901579-A1.
XX 14-JAN-1999.
XX 01-JUL-1998; 98WO-US13574.
XX 01-JUL-1997; 97US-0886829.
XX (ISIS-) ISIS PHARM INC.
XX Hardee G, Teng C;
XX WPI, 1999-106077/09.
XX

PT Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides
 PT across the gastrointestinal mucosa, provides high bioavailability
 XX
 PS Example 2; Page 83; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a
 CC nucleic acid and at least one penetration enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder that can be
 CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
 CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, in human or animal medicine;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-35%. The penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AAX18669 to AAX18799 and AAX18801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.

SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgctgcg 17
 |||
 DB 2 cctctaccgcgctgcg 18

RESULT 9

AAZ49348
 ID AAZ49348 standard; DNA: 20 BP.

XX AAZ49348;

DT 14-MAR-2000 (first entry)

DE bcl-2 targeted antisense oligonucleotide SEQ ID 13.

KW Cellular proliferation; expression; modulation; antisense;

KW non-parenteral; delivery; uptake; administration; emulsion;

KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;

SS.

OS Synthetic.

OS Homo sapiens.

PN WO960012-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US11394.

PR 21-MAY-1998; 98US-0082624.

PA (ISIS-) ISIS PHARM INC.

PI Teng C, Cook PD, Tillman L, Hardee GE, Ecker DJ, Manoharan M;

DR WPI; 2000-072428/06.

XX New oligonucleotide compositions used for the non-parenteral delivery
 PT of e.g. antisense oligos, ribozymes, peptide nucleic acids, molecular
 PT decoys, external guide sequences or aptamers
 XX Example 2; Page 122; 133pp; English.

CC Sequences AAZ49344-249354, AAZ49384-249385, AAZ49387-249388 and
 CC AAZ49392-249393 represent antisense oligonucleotides designed
 CC to modulate the rate of cellular proliferation. The invention relates to
 CC new compositions for the non-parenteral delivery of oligonucleotides
 CC comprising at least one oligonucleotide in an emulsion. Oligonucleotides
 CC delivered via the compositions of the invention can be used to modulate
 CC expression of a cellular adhesion protein, modulate a rate of cellular
 CC proliferation, or have biological activity against eukaryotic pathogens
 CC or retroviruses. They can be used for treating conditions including
 CC e.g., ulcerative colitis, Crohn's disease, inflammatory bowel disease
 CC or undue cellular proliferation. The compositions can enhance the local
 CC and systemic uptake and delivery of nucleic acids via non-parenteral
 CC routes of administration (e.g., via the alimentary canal, skin, eyes,
 CC pulmonary tract, urethra or vagina).

SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 21; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctaccgcgctgcg 17
 |||
 DB 2 cctctaccgcgctgcg 18

RESULT 10

AAQ86652
 ID AAQ86652 standard; DNA: 17 BP.

XX AAQ86652;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticancer oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW lymphoma; programmed cell death; ss.

OS Synthetic.

FT Key Location/Qualifiers

FT misc_feature 1..17

FT /tag= a /note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumours, esp. breast cancer
 PT
 XX Example 12; Page 33; 108pp; English.

XX Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS11846. The oligonucleotides are phosphodiester targeted
 CC against the translation initiation site (AAQ86650-55) or the 5'-cap
 CC region (AAQ86656-58) of human bcl-2 pre-mRNAs. The AAQ86652
 CC oligonucleotide provided pronounced DNA fragmentation.

SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctaccgcgtgcg 17
|||||
Db 1 tctaccgcgtgcg 14

RESULT 11

AA086654 standard; DNA; 17 BP.

XX AA086654;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KW Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW Lymphoma; programmed cell death; ss.

OS Synthetic.

EH Key location/Qualifiers

FT misc.feature 1..17
/tag= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

XX Reed JC;

DR WPI; 1995-139394/18.

PT Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce

CC programmed cell death (DNA fragmentation) in the human lymphoma cell

CC line RS11846. The oligonucleotides are phosphodiester targeted

CC against the translation initiation site (AA086650-55) or the 5'-cap

CC region (AA086656-58) of human bcl-2 pre-mRNAs.

XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccttcctaccgcgt 14
|||||

Db 4 ccttcctaccgcgt 17

RESULT 12

AAV28173

ID AAV28173 standard; DNA; 17 BP.

AC AAV28173;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

PI Chen D, Cole DL, Srivatsa GS;

DR WPI; 1998-362922/31.

PT Matrix for selective separation of oligo:nucleotide - useful for,

PT e.g. large scale purification of anti-sense agents from their

PT deletion derivatives formed during synthesis

PS Disclosure; Page 79; 183pp; English.

CC AAV28155-268 represent oligonucleotides which can be purified using the

CC method of the invention. The specification describes a matrix that

CC comprises a support and an affinity unit that specifically and

CC reversibly binds a target oligonucleotide, and comprises a sequence of

CC bases having the reverse complement of a hybridising portion of the

CC target oligonucleotide. The matrix is used for affinity purification of

CC synthetic oligonucleotides, specifically antisense agents, for treatment

CC of hyperproliferative diseases, for treating a non-pathogen,

CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating

CC expression of cell surface proteins, and to inhibit a eukaryotic

CC pathogen, retrovirus or other viruses.

XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctaccgcgtgcg 17
|||||

Db 1 tctaccgcgtgcg 14

RESULT 13

AAV28174 standard; DNA; 17 BP.

AAV28174;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

KW Purification; oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

PD 25-JUN-1998.

XX 18-DEC-1997; 97WO-US23284.
PF
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
PI Chen D, Cole DL, Srivatsa GS;
XX WPI; 1998-362922/31.
DR
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 80; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 tctctaccgcgtcgcg 17
|||||
Db 1 tctctaccgcgtcgcg 14

RESULT 14
AAV28176
ID AAV28176 standard; DNA; 17 BP.
XX
AC AAV28176;
XX
DT 08-OCT-1998 (first entry)
XX
DE Antisense oligonucleotide to bcl-2 mRNA.
XX
XX Purification; oligonucleotide; matrix; affinity unit;
KM affinity purification; antisense; bcl-2; ss.
XX
OS Synthetic.
XX
PN WO9827425-A1.
XX
PD 25-JUN-1998.
XX
PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
PI Chen D, Cole DL, Srivatsa GS;
XX WPI; 1998-362922/31.
DR
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis

XX Disclosure; Page 82; 183pp; English.
PS
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 cctctctaccgcgt 14
|||||
Db 4 cctctctaccgcgt 17

RESULT 15
AAV23688
ID AAV23688 standard; DNA; 17 BP.
XX
AC AAV23688;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 141.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
XX
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
PI Chen D, Srivatsa GS;
XX WPI; 1999-205198/17.
DR
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
PS Example 9; Page 150; 163pp; English.

XX
CC This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical

CC compositions that are useful for modulating cellular adhesion or
 CC proliferation, and being active against a eukaryotic pathogen, a human
 CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
 CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
 CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
 CC characterization of deletion sequence oligonucleotides having related,
 CC but different nucleobase sequences, and quantification of different
 CC species of deletion sequence ("target") oligonucleotides in a mixture.
 CC Also, if the specificity of the oligonucleotide's nucleobase sequence
 CC for its reverse complement is not modified, the method may be performed
 CC using oligodeoxynucleotides.

XX
 SQ Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccttcctaccgcgt 14
 ||||||||||||
 Db 4 ccttcctaccgcgt 17

Search completed: June 28, 2002, 22:40:14
 Job time: 8090 sec

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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:47 ; Search time 334.55 seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-11

Perfect score: 17

Sequence: 1 cctctaccgcgtgcg 17

Scoring table: IDENTITY NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTNUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-465-485A-11
2	17	100.0	17	3	US-09-080-285-11
3	14	82.4	17	2	US-08-465-485A-10
4	14	82.4	17	2	US-08-465-485A-12
5	14	82.4	17	3	US-09-080-285-10
6	14	82.4	17	3	US-09-080-285-12
7	12.2	71.8	37	3	US-09-403-267-23
8	11.8	69.4	24	3	US-08-744-550-1
9	11.8	69.4	24	3	US-09-160-671-1
10	11.8	69.4	26	4	US-09-094-557-19
11	11.8	69.4	28	4	US-09-094-557-21
12	11.8	69.4	28	4	US-09-094-557-26
13	11.8	69.4	66	2	US-08-185-949B-85
14	11.4	67.1	28	4	US-08-870-930-56
15	11.4	67.1	28	4	US-08-870-930-57
16	11.4	67.1	29	4	US-08-870-930-74
17	11.4	67.1	29	4	US-08-870-930-75
18	11.4	67.1	29	4	US-08-870-930-76
19	11.4	67.1	29	4	US-08-870-930-77
20	11.4	67.1	30	4	US-08-870-930-55
21	11.4	67.1	61	4	US-08-870-930-17
22	11.4	67.1	61	4	US-08-870-930-22
23	11.4	67.1	61	4	US-08-870-930-56
24	11.2	65.9	22	3	US-09-275-850-33
25	11.2	65.9	24	4	US-07-912-122-1
26	11.2	65.9	24	5	PCT-US93-06404-1
27	11.2	65.9	28	2	US-08-859-998-111

28	11.2	65.9	28	4	US-09-225-928-111	Sequence 111, App
29	11.2	65.9	33	5	PCT-US95-04583-2	Sequence 2, Appl
30	11.2	65.9	45	2	US-08-450-905B-38	Sequence 38, Appl
31	11.2	65.9	45	3	US-07-982-759F-38	Sequence 38, Appl
32	11.2	65.9	60	1	US-08-484-192-154	Sequence 154, App
33	11	64.7	17	2	US-08-465-485A-9	Sequence 9, Appl
34	11	64.7	17	2	US-08-465-485A-13	Sequence 13, Appl
35	11	64.7	17	3	US-09-080-285-13	Sequence 13, Appl
36	11	64.7	17	3	US-09-080-285-13	Sequence 13, Appl
37	11	64.7	18	4	US-09-030-701-28	Sequence 28, Appl
38	11	64.7	18	4	US-09-286-098-60	Sequence 60, Appl
39	11	64.7	18	4	US-08-960-774-60	Sequence 60, Appl
40	11	64.7	23	4	US-08-870-930-58	Sequence 58, Appl
41	11	64.7	23	4	US-08-870-930-84	Sequence 84, Appl
42	11	64.7	57	3	US-09-135-639-7	Sequence 7, Appl
43	11	64.7	57	3	US-09-135-639-9	Sequence 9, Appl
44	10.8	63.5	15	1	US-08-291-932A-329	Sequence 329, App
45	10.8	63.5	18	3	US-09-199-859-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-465-485A-11
Sequence 11, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIYAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-11

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctgctg 17
|||||
DB 1 CCTTCTACCGCGTGG 17

RESULT 2

US-09-080-285-11
; Sequence 11, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-11

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cctctaccgctgctg 17
|||||
DB 1 CCTTCTACCGCGTGG 17

RESULT 3

US-08-465-485A-10
; Sequence 10, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-10

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tctctaccgctgctg 17
|||||
DB 1 TCTTACCGCGTGG 14

RESULT 4

US-08-465-485A-12
; Sequence 12, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-12

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ccttcaccgcgt 14
|||||
Db 4 CCTTCCCTACCGCGT 17

RESULT 5
US-09-080-285-10
Sequence 10, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-10

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 tcttcaccgcgtgcg 17
|||||
Db 1 TCCTACCGCGTGC 14

RESULT 6
US-09-080-285-12
Sequence 12, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-12

Query Match
Best Local Similarity 82.4%; Score 14; DB 3; Length 17;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ccttcctaccgct 14
|||||
DB 4 CCTTCCTACCGCT 17

RESULT 7
US-09-403-267-23
Sequence 23, Application US/09403267
Patent No. 6159710
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy, and Biology
APPLICANT: Fraser, Nigel W.
APPLICANT: Zabolotny, Janice M.
APPLICANT: Krummenacher, Claude F.
TITLE OF INVENTION: Method and Compositions for Stabilizing
TITLE OF INVENTION: Unstable Gene Transcripts
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., P.O. Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/403,267
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/044,664
FILING DATE: 18-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST78APCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:

LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "probe/primer PPPB8"
US-09-403-267-23

Query Match
Best Local Similarity 71.8%; Score 12.2; DB 3; Length 37;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 ccttcctaccgctg 17
|||||
DB 6 CCTTCCTACCGCGGC 22

RESULT 8
US-08-744-590-1
Sequence 1, Application US/08744590
Patent No. 6074823
GENERAL INFORMATION:
APPLICANT: Koster, Hubert
TITLE OF INVENTION: DNA Sequencing By Mass Spectrometry Via
TITLE OF INVENTION: Exonuclease Degradation
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,590
FILING DATE: No. 6074823ember 6, 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/388,171
FILING DATE: February 10, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/034,738
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: SCI-005CNCNP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-744-590-1

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 3; Length 24;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ccttcctaccgctg 15
|||||
DB 3 CATTCCTACCGCGTG 17

RESULT 9
US-09-160-671-1
; Sequence 1, Application US/09160671
; Patent No. 6140053
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; TITLE OF INVENTION: DNA SEQUENCING BY MASS SPECTROMETRY VIA
; TITLE OF INVENTION: EXONUCLEASE DEGRADATION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Edman White & Mcauliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/160,671
; FILING DATE: 25-SEP-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/388,272,744,590
; FILING DATE: 10-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/034,738
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2005B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-450-8499
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-160-671-1

Query Match 69.4%; Score 11.8; DB 3; Length 24;
Best Local Similarity 86.7%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ccttcctaccgctg 15
1 ||||| |||||
Db 3 CATTCACCGCGTGC 17

RESULT 10
US-09-094-557-19/c
; Sequence 19, Application US/09094557
; Patent No. 6225531
; GENERAL INFORMATION:
; APPLICANT: Kakitani, Makoto
; APPLICANT: Umemoto, Naoyuki
; APPLICANT: Ishida, Isao
; APPLICANT: Iwamatsu, Akihiro
; APPLICANT: Yoshikawa, Masaaki

APPLICANT: Yamaoka, Naoto
TITLE OF INVENTION: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH
TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03653
FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 136100/1994
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 347823/1995
FILING DATE: 15-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-094-557-19

Query Match 69.4%; Score 11.8; DB 4; Length 26;
Best Local Similarity 86.7%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 cttctaccgctgc 16
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Db 26 CTTCTACCGCATGC 12

RESULT 11
US-09-094-557-21
; Sequence 21, Application US/09094557
; Patent No. 6225531
; GENERAL INFORMATION:
; APPLICANT: Kakitani, Makoto
; APPLICANT: Umemoto, Naoyuki
; APPLICANT: Ishida, Isao
; APPLICANT: Iwamatsu, Akihiro
; APPLICANT: Yoshikawa, Masaaki
; APPLICANT: Yamaoka, Naoto
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH

TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03653
FILING DATE: 13-DEC-1996
APPLICATION DATA:
APPLICATION NUMBER: JP 136100/1994
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 347823/1995
FILING DATE: 15-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-094-557-21

Query Match 69.4%; Score 11.8; DB 4; Length 28;
Best Local Similarity 86.7%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctctaccgcgtgc 16
|||||
DB 11 CTCTCTACCCCATGC 25

RESULT 12
US-09-094-557-26
Sequence 26, Application US/09094557
Patent No. 6225531
GENERAL INFORMATION:
APPLICANT: Kakitani, Makoto
APPLICANT: Umemoto, Naoyuki
APPLICANT: Ishida, Isao
APPLICANT: Iwamatsu, Akihito
APPLICANT: Yoshikawa, Masaaki
APPLICANT: Yamaoka, Naoto
TITLE OF INVENTION: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE
TITLE OF INVENTION: CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH
TITLE OF INVENTION: THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,557
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03653
FILING DATE: 13-DEC-1996
APPLICATION DATA:
APPLICATION NUMBER: JP 136100/1994
FILING DATE: 17-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 347823/1995
FILING DATE: 15-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/591,566
FILING DATE: 14-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 081356/0116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-094-557-26

Query Match 69.4%; Score 11.8; DB 4; Length 28;
Best Local Similarity 86.7%; Pred. No. 7.1e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ctctctaccgcgtgc 16
|||||
DB 11 CTCTCTACCCCATGC 25

RESULT 13
US-08-185-949B-85
Sequence 85, Application US/08185949B
Patent No. 5874279
GENERAL INFORMATION:
APPLICANT: Mark D. Cochran
APPLICANT: Richard D. Macdonald
TITLE OF INVENTION: Recombinant Infectious Bovine
TITLE OF INVENTION: Rhinotracheitis Virus
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM 330 466 DX2
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,949B
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0525
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-185-949B-85

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 2; Length 66;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ttctctaccgctgcg 17
|||||
Db 14 ttctctaccgctgcg 28

RESULT 14
US-08-870-930-56/c
Sequence 56, Application US/08870930
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGESE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA

FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
US-08-870-930-56

Query Match
Best Local Similarity 67.1%; Score 11.4; DB 4; Length 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctctctaccgct 14
|||||
Db 17 ctctctaccgcat 5

RESULT 15
US-08-870-930-57/c
Sequence 57, Application US/08870930
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGESE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
FEATURE:
OTHER INFORMATION: C in position 28 is 2'-OH C
US-08-870-930-57

Query Match
Best Local Similarity 67.1%; Score 11.4; DB 4; Length 28;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ctctctaccgct 14
|||||
Db 16 ctctctaccgcat 4

Search completed: June 28, 2002, 22:16:48
Job Time: 8274 sec

Mon Jul 1 08:40:46 2002

us-09-709-170a-11.szlm75.rni

Query Match	100.0%;	Score 17;	DB 6;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 56;		

1	17	100.0	17	6	AR052613	AR052614	Sequence
2	14	82.4	17	6	AR052613	AR052613	Sequence
3	14	82.4	17	6	AR052615	AR052615	Sequence
4	12.4	72.9	47	6	AR050327	AR050327	Sequence
5	12.4	72.9	47	6	HUMTCGVJ32	L39499	Homo sapien
6	12.4	72.9	52	9	S63038	S63038	T cell rece
7	12.2	71.8	51	6	AX204129	AX204129	Sequence
8	12.2	71.8	67	6	AR081385	AR081385	Sequence
9	12	70.6	47	9	HUMTCVDBHQ	L32414	Human (clon
10	11.8	69.4	21	6	AX012319	AX012319	Sequence
11	11.8	69.4	25	6	AX022216	AX022216	Sequence
12	11.8	69.4	25	6	AX030742	AX030742	Sequence
13	11.8	69.4	35	6	BD08657	BD08657	Strable ex
14	11.8	69.4	30	6	AR125801	AR125801	Sequence
15	11.8	69.4	30	6	AR125805	AR125805	Sequence
16	11.8	69.4	30	6	147213	147213	Sequence
17	11.8	69.4	30	6	147217	147217	Sequence
18	11.8	69.4	30	6	AX202434	AX202434	Sequence
19	11.8	69.4	50	6	AX202434	AX202434	Sequence
20	11.8	69.4	60	10	AF265815	AF265815	Mus muscu
21	11.8	69.4	72	9	HUMTCGD2B	M28772	Human T-cell
22	11.4	67.1	18	12	AMM292027	AJ229027	Artificia
23	11.4	67.1	20	6	BD009422	BD009422	Probes, m
24	11.4	67.1	28	6	AR122834	AR122834	Sequence
25	11.4	67.1	28	6	AR122835	AR122835	Sequence
26	11.4	67.1	29	6	AR122852	AR122852	Sequence
27	11.4	67.1	29	6	AR122853	AR122853	Sequence
28	11.4	67.1	29	6	AR122854	AR122854	Sequence
29	11.4	67.1	29	6	AR122855	AR122855	Sequence
30	11.4	67.1	30	6	AR122855	AR122855	Sequence
31	11.4	67.1	32	6	AR026317	AR026317	Sequence
32	11.4	67.1	55	6	AR172872	AR172872	Sequence
33	11.4	67.1	55	6	AX057560	AX057560	Sequence
34	11.4	67.1	55	6	HUMTCVDFJ	L32511	Human (clon
35	11.4	67.1	59	9	HUMTCVDFJ	L32511	Human (clon
36	11.4	67.1	61	6	AR122795	L39615	Homo sapien
37	11.4	67.1	61	6	AR122800	AR122795	Sequence
38	11.4	67.1	62	6	AX193276	AX122800	Sequence
39	11.4	67.1	62	6	AX193441	AX133276	Sequence
40	11.4	67.1	67	6	AX193327	AX193327	Sequence
41	11.4	67.1	67	6	AX193345	AX193345	Sequence
42	11.4	67.1	69	6	AX192906	AX192906	Sequence
43	11.4	67.1	70	6	AX192919	AX182919	Sequence
44	11.2	65.9	24	6	AX290793	AX290793	Sequence
45	11.2	65.9	26	6	A20104	A20104	protease B

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgct 17
|||||
Db 1 GACCTTCTACCGCT 17

RESULT 2
AR052613 AR052613 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 11 from patent US 5831066.
DEFINITION AR052613
ACCESSION AR052613
VERSION AR052613.1 GI:5975977
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 11 03-NOV-1998;
FEATURES Location/Qualifiers
Source 1.17
/organism="unknown"

BASE COUNT 1 a 8 c 4 g 4 t

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ccttcctaccgct 17
|||||
Db 1 CCTTCTACCGCT 14

RESULT 3
AR052615 AR052615 17 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 13 from patent US 5831066.
DEFINITION AR052615
ACCESSION AR052615
VERSION AR052615.1 GI:5975979
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 13 03-NOV-1998;
FEATURES Location/Qualifiers
Source 1.17
/organism="unknown"

BASE COUNT 3 a 7 c 4 g 3 t

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccg 14
|||||
Db 4 GACCTTCTACCG 17

RESULT 4
AR050327 AR050327 40 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 17 from patent US 5827684.
DEFINITION AR050327
ACCESSION AR050327
VERSION AR050327.1 GI:5973052

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 40)
AUTHORS Sreekrishna,K., Prevatt,W.D., Thill,G.P., Davis,G.R., Koutz,P.,
Barr,K.A. and Hopkins,S.A.
TITLE Production of Bacillus entomotoxins in methylotrophic yeast
JOURNAL Patent: US 5827684-A 17 27-OCT-1998;
FEATURES Location/Qualifiers
Source 1.40
/organism="unknown"

BASE COUNT 11 a 8 c 10 g 11 t

Query Match 72.9%; Score 12.4; DB 6; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gaccctctaccg 14
|||||
Db 40 GACCTTCTACCG 27

RESULT 5
HMMTCGVJ32 47 bp mRNA linear PRI 19-AUG-1995
LOCUS Homo sapiens (C.2.PL252) rearranged T-cell receptor delta chain
DEFINITION (TCRDV2J1) mRNA, partial V-region.
ACCESSION L39499
VERSION L39499.1 GI:945251
KEYWORDS CDR3 region; T-cell receptor alpha-chain; T-cell receptor delta;
antigen recognition site; junctional region; rearranged; variable
region.
SOURCE Homo sapiens (clone: C.2.PL252) colon CDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 47)
Holtmeier W., Chowers,Y., Lumeng,A., Morzycka-Wroblewska,E. and
Kagnoff,M.F.
TITLE The delta T cell receptor repertoire in human colon and peripheral
blood is oligoclonal irrespective of V region usage
JOURNAL J. Clin. Invest. 96 (2), 1108-1117 (1995)
COMMENT Citation paper.
FEATURES Location/Qualifiers
Source 1.47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C.2.PL252"
/tissue.type="colon"
<1..>47
/gene="TCRDV2J1"
/standard_name="(V delta-2/ J delta-1)"
/note="putative"
1..47
/gene="TCRDV2J1"
<1..>47
/note="This CDS feature is included to show the
translation of the corresponding V-region. Presently
translation qualifiers on V-region features are illegal."
/codon_start=1
/protein_id="AAC41800.1"
/db_xref="GI:950449"
/translation="ACDTLPALPNAYKL"
BASE COUNT 12 a 6 g 10 t
ORIGIN 19 c 6 g 10 t

Query Match 72.9%; Score 12.4; DB 9; Length 47;

Best Local Similarity 92.9%; Pred. No. 2.6e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 acccttcctaccgc 15
|||||

Db 10 ACCCTTCTACGCGT 23

RESULT 6

LOCUS S63038 52 bp DNA linear PRI 25-AUG-1993
DEFINITION T cell receptor V delta 1-J delta 1 junction [sample 127] (human,
adult, Genomic, 52 nt).

ACCESSION S63038

VERSION S63038.1 GI:386400

KEYWORDS human adult.

SOURCE

ORGANISM

Human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 52)
Bejdjordi, K., Bejdjordi, C., Macintyre, E., Even, P. and Sigaux, F.
Peripheral selection of V delta 1+ cells with restricted T cell
receptor delta gene repertoire in the peripheral blood
of healthy donors

J. Exp. Med. 178 (1), 121-127 (1993)

JOURNAL

MEDLINE

REMARK

Genbank staff at the National Library of Medicine created this
entry [NCBI gidsq 134205] from the original journal article.
This sequence comes from Fig. 2.

FEATURES

source 1..52
/organism="Homo sapiens"
/db_xref="taxon:9606"

gene

partial

/gene="T cell receptor V delta 1-J delta 1 junction"
1..52
17 c 11 g 14 t

BASE COUNT

ORIGIN

Query Match 72.9%; Score 12.4; DB 9; Length 52;
Best Local Similarity 92.9%; Pred. No. 2.6e+04;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 ccttcctaccgcgt 17
|||||

Db 20 CCTTCTACGCGGT 33

RESULT 7

LOCUS AX204129 51 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 235 from Patent WO0148245.

ACCESSION AX204129

VERSION AX204129.1 GI:15393623

KEYWORDS human.

SOURCE

ORGANISM

Human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 51)
Shinkets, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
Patent: WO 0148245-A 235 05-JUL-2001;

JOURNAL

FEATURES

source 1..51
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"

variation

/note="single nucleotide polymorphism

BASE COUNT 8 a 19 c 16 g 8 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 51;
Best Local Similarity 82.4%; Pred. No. 3.4e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gacccttcctaccgcgt 17
|||||

Db 28 GACCTTCTACGCGT 44

RESULT 8

LOCUS AR081385 67 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 44 from patent US 5972599.

ACCESSION AR081385

VERSION AR081385.1 GI:10008111

KEYWORDS Unknown.

SOURCE

ORGANISM

Unclassified.
1 (bases 1 to 67)
Tasset, P., Pagratidis, N., Jayasena, S. and Gold, L.
High affinity nucleic acid ligands of cytokines
Patent: US 5972599-A 44 26-OCT-1999;

JOURNAL

FEATURES

source 1..67
/organism="unknown"

BASE COUNT 13 a 13 c 29 g 12 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 6; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.3e+04;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gacccttcctaccgcgt 17
|||||

Db 44 GACCTTCTACGCGT 28

RESULT 9

LOCUS HUMTCVD1BQ 47 bp mRNA linear PRI 10-FEB-1995
DEFINITION Human (clone: 1st1p131) T-cell receptor delta-chain (V-delta-1)
mRNA.

ACCESSION U32414

VERSION U32414.1 GI:497484

KEYWORDS T-cell receptor; delta chain.

SOURCE

ORGANISM

Human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 47)
Kagano, Y., Holtmeier, W., Harwood, J., Morzycka-Wroblewska, E. and
Chowers, Y.F.
The V delta 1 T cell receptor repertoire in human small intestine
and colon

J. Exp. Med. 180 (1), 183-190 (1994)

JOURNAL

MEDLINE

FEATURES

source 1..47
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="intestine"

BASE COUNT 10 a 15 c 12 g 10 t
ORIGIN

Query Match 70.6%; Score 12; DB 9; Length 47;

Best Local Similarity 100.0%; Pred. No. 4.5e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gaccctctctac 12
|||||
Db 9 GACCTTCTCTAC 20

RESULT 10
AX012319/c 21 bp DNA linear PAT 06-SEP-2000
LOCUS
DEFINITION Sequence 7 from Patent WO955316.
ACCESSION AX012319
VERSION AX012319.1 GI:9998368
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 21)
AUTHORS Wiese,M.
TITLE Kinase obtained from leishmania
JOURNAL Patent: WO 995316-A 7 04-NOV-1999;
MAX PLANCK GESELLSCHAFT (DE); WIESE MARTIN (DE)
FEATURES
source 1..21
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR-Primer"

BASE COUNT 5 a 3 c 10 g 3 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 21;
Best Local Similarity 86.7%; Pred. No. 6.3e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 ccctctaccgcgt 17
|||||
Db 17 CCTTCGACCCCGT 3

RESULT 11
AX022216/c 25 bp DNA linear PAT 07-SEP-2000
LOCUS
DEFINITION Sequence 23 from Patent EP0950098.
ACCESSION AX022216
VERSION AX022216.1 GI:10045876
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: EP 0950098-A 23 20-OCT-1999;
COMM SCIENT IND RES ORG (AU)
FEATURES
source 1..25
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 3 a 5 c 13 g 4 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 6.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctctaccgcg 16
|||||
Db 17 ACCCTTACACCGCG 3

RESULT 12
AX030742/c 25 bp DNA linear PAT 20-SEP-2000
LOCUS
DEFINITION Sequence 23 from Patent WO9818918.
ACCESSION AX030742
VERSION AX030742.1 GI:10278250
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Ramshaw,J.A., Galanis,M., Vaughan,P.R. and Werkmeister,J.A.
TITLE Stable expression of triple helical proteins
JOURNAL Patent: WO 9818918-A 23 07-MAY-1998;
RAMSHAW JOHN ALAN MAURICE (AU); GALANIS MARIA (AU); COMM SCIENT
IND RES ORG (AU); VAUGHAN PAUL RICHARD (AU); WERKMEISTER JEROME
ANTHONY (AU)
FEATURES
source 1..25
Location/Qualifiers
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 3 a 5 c 13 g 4 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 6.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 accctctaccgcg 16
|||||
Db 17 ACCCTTACACCGCG 3

RESULT 13
BD008657/c 25 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Stable expression of the triple helical protein.
ACCESSION BD008657
VERSION BD008657.1 GI:18637030
KEYWORDS JP 2001502548-A/17.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Vaughan,P.R., Galanis,M., Ramshaw,J.A.M. and Werkmeister,J.A.
TITLE Stable expression of the triple helical protein
JOURNAL Patent: JP 2001502548-A 17 27-FEB-2001.
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
COMMENT OS Unidentified
PN JP 2001502548-A/17
PD 27-FEB-2001
PF 29-OCT-1997 JP 1998519817
PR PAUL RICHARD VAUGHAN, MARIA GALANIS, JOHN ALAN MAURICE RAMSHAW,
PI JEROME ANTHONY WERKMEISTER
PC C12N15/12, C12N15/81, C12N15/53, C07K14/78, A61K38/39 CC
Strandedness: Single;
CC Topology: Linear;
FH key
FT source 1..25
Location/Qualifiers
/organism="unidentified"

BASE COUNT 3 a 5 c 13 g 4 t
ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 25;
Best Local Similarity 86.7%; Pred. No. 6.2e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acccttctaccgcg 16
 ||||| |||||
 Db 17 ACCCTTACCAACCCGC 3

RESULT 14
 ARI25801 30 bp DNA linear PAT 16-MAY-2001
 LOCUS ARI25801/c
 DEFINITION Sequence 143 from patent US 6177557.
 ACCESSION ARI25801
 VERSION ARI25801.1 GI:14111863
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 30)
 AUTHORS Janjic,N., Gold,L., and Tasset,D.
 TITLE High affinity ligands of basic fibroblast growth factor and thrombin
 JOURNAL Patent: US 6177557-A 143 23-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..30
 /organism="unknown"
 BASE COUNT 5 a 4 c 17 g 4 t
 ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 30;
 Best Local Similarity 86.7%; Pred. No. 6.1e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acccttctaccgcg 16
 ||||| |||||
 Db 27 ACCCATCTACCCCG 13

RESULT 15
 ARI25805/c 30 bp DNA linear PAT 16-MAY-2001
 LOCUS ARI25805
 DEFINITION Sequence 147 from patent US 6177557.
 ACCESSION ARI25805
 VERSION ARI25805.1 GI:14111867
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

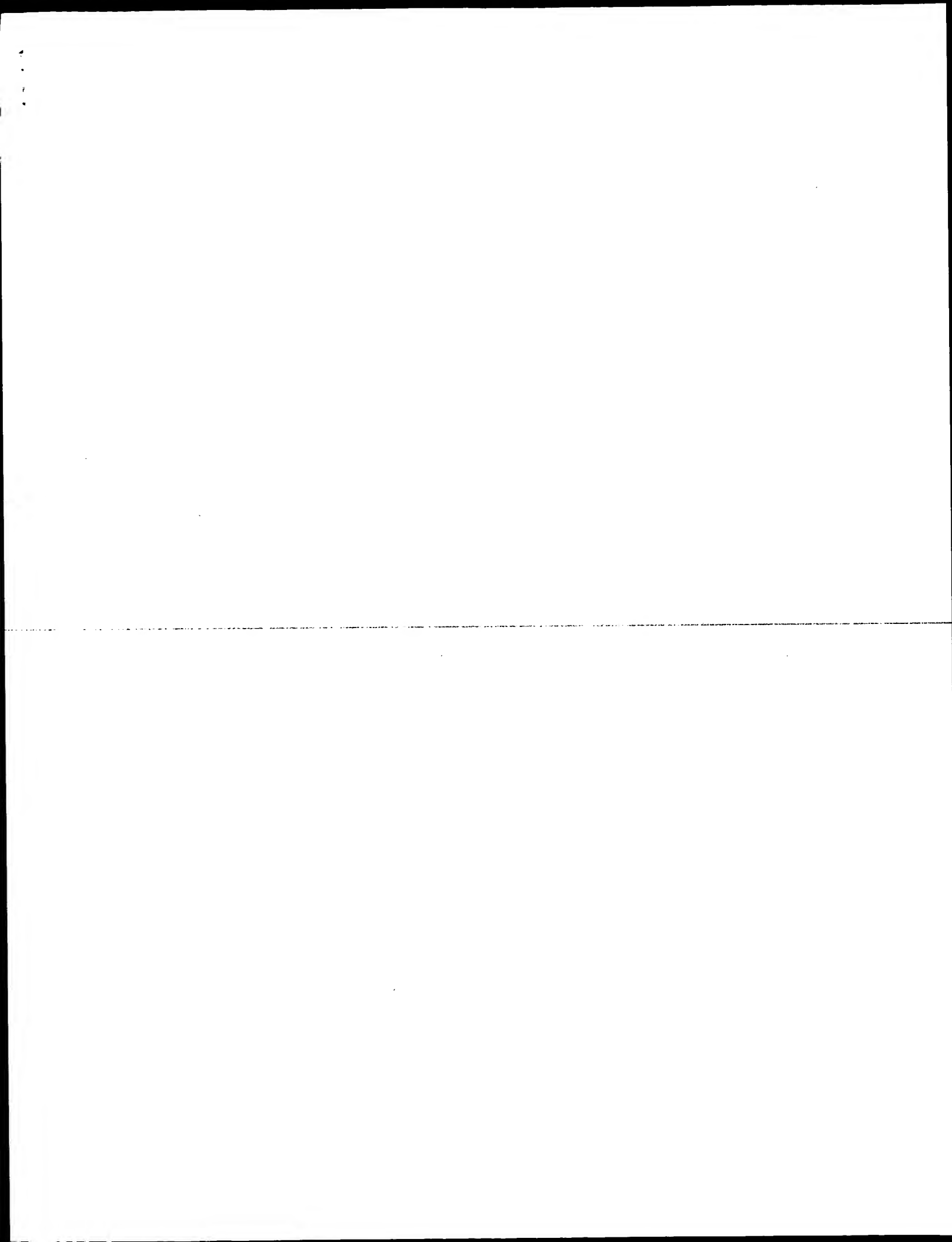
REFERENCE 1 (bases 1 to 30)
 AUTHORS Janjic,N., Gold,L., and Tasset,D.
 TITLE High affinity ligands of basic fibroblast growth factor and thrombin
 JOURNAL Patent: US 6177557-A 147 23-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..30
 /organism="unknown"

BASE COUNT 5 a 4 c 17 g 4 t
 ORIGIN

Query Match 69.4%; Score 11.8; DB 6; Length 30;
 Best Local Similarity 86.7%; Pred. No. 6.1e+04;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acccttctaccgcg 16
 ||||| |||||
 Db 27 ACCCATCTACCCCG 13

Search completed: June 28, 2002, 22:11:11
 Job time: 8362 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:14 ; Search time 1381.16 Seconds

(without alignments)
21.133 Million cell updates/sec

Title: US-09-709-170A-12

Perfect score: 17

Sequence: 1 gaccctctaccgcgt 17

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N.Geneseq_032802:*

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2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

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4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

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9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

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19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

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22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	16	AAQ86654
2	17	100.0	17	19	AAV28176
3	17	100.0	17	20	AAV23688
4	17	100.0	17	20	AAQ86697
5	15	88.2	20	16	AAQ86643
6	15	88.2	20	19	AAV28169
7	15	88.2	20	20	AAV23681
8	15	88.2	20	20	AAV18690
9	15	88.2	20	21	AAV29348

10	14	82.4	17	16	AAQ86653	Bcl-2 antisense ol
11	14	82.4	17	16	AAQ86655	Bcl-2 antisense ol
12	14	82.4	17	19	AAV28175	Antisense oligonuc
13	14	82.4	17	19	AAV28177	Antisense oligonuc
14	14	82.4	17	20	AAV23687	Deletion sequence
15	14	82.4	17	20	AAV23689	Deletion sequence
16	14	82.4	17	20	AAV18696	Target bcl-2 antis
17	14	82.4	17	20	AAV18698	Target bcl-2 antis
18	14	82.4	19	17	AAV27370	Anti-ras oncogene
19	12.2	71.8	27	19	AAV63985	Mycobacterium tube
20	12.2	71.8	27	20	AAV81049	PCR primer for clo
21	12.2	71.8	37	18	AAV87143	IFN-gamma 2'NH2 RN
22	12.2	71.8	51	22	AAH79620	Human DNA containi
23	11.8	69.4	17	21	AAH70263	Hammerhead ribozym
24	11.8	69.4	17	21	AAH70263	Hammerhead ribozym
25	11.8	69.4	21	21	AAZ24128	L. mexicana lmpk p
26	11.8	69.4	25	19	AAV27135	Synthetic human co
27	11.8	69.4	30	16	AAQ83300	Two member family
28	11.8	69.4	30	16	AAQ83304	bFGF 2'-NH2 RNA II
29	11.8	69.4	30	22	AAV57460	Arabidopsis acyltr
30	11.8	69.4	30	22	AAV70681	2'NH2 RNA ligand t
31	11.8	69.4	40	21	AAZ96153	2'NH2 RNA ligand t
32	11.8	69.4	50	22	AAV11596	Polynucleotide seq
33	11.8	69.4	50	22	AAV11596	Non-target oligo N
34	11.4	67.1	20	19	AAV73521	Non-target oligo N
35	11.4	67.1	20	19	AAV73521	H. pylori vaca pri
36	11.4	67.1	20	20	AAV05149	PCR primer used to
37	11.4	67.1	32	20	AAV55589	Primer for Ngp II
38	11.4	67.1	36	21	AAV35739	Permutin linker e
39	11.4	67.1	51	22	AAV32896	Human SNP oligonuc
40	11.4	67.1	55	22	AAV81393	Rat GLUT4/myc epit
41	11.4	67.1	61	21	AAV69861	VEGF-binding nucle
42	11.4	67.1	62	22	AAI29289	Colon tumour relat
43	11.4	67.1	62	22	AAI29454	Colon tumour relat
44	11.4	67.1	67	22	AAI29340	Colon tumour relat
45	11.4	67.1	67	22	AAI29358	Colon tumour relat

ALIGNMENTS

RESULT 1	
AAQ86654	AAQ86654 standard; DNA; 17 BP.
XX	
AC	AAQ86654:
XX	
DT	27-SEP-1995 (first entry)
XX	
DE	Bcl-2 antisense oligonucleotide.
XX	
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW	Lymphoma; programmed cell death; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	misc_feature
FT	Location/Qualifiers
FT	1..17
FT	/tag= a
FT	/note= "3'-5' (antisense) sequence"
XX	
PN	WO9508350-A.
XX	
PD	30-MAR-1995.
XX	
PF	20-SEP-1994; 94WO-US10725.
XX	
PR	20-SEP-1993; 93US-0124256.
XX	
PA	(REED/) REED J C.
XX	
PI	Reed JC;
XX	

DR WPI; 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX Example 12; Page 33; 108pp; English.
XX Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS11846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaccctctaccgcgt 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 gaccctctaccgcgt 17

RESULT 2
AAV28176
ID AAV28176 standard; DNA; 17 BP.
XX
XX AAV28176;
XX
XX 08-OCT-1998 (first entry)
XX
XX Antisense oligonucleotide to bcl-2 mRNA.
DE
XX Purification; oligonucleotide; matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO9827425-A1.
PN
XX
XX 25-JUN-1998.
PD
XX
XX 18-DEC-1997; 97WO-US23284.
PF
XX
XX 19-DEC-1996; 96US-0769951.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Chen D, Cole DL, Srivatsa GS;
PI
XX
XX WPI; 1998-362922/31.
DR
XX
XX Matrix for selective separation of oligonucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX
XX Disclosure; Page 82; 183pp; English.
PS
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative diseases, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaccctctaccgcgt 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 gaccctctaccgcgt 17

RESULT 3
AAV23688
ID AAV23688 standard; DNA; 17 BP.
XX
XX AAV23688;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 141.
DE
XX
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
KW
XX
XX Synthetic.
OS
XX
XX WO9911820-A1.
PN
XX
XX 11-MAR-1999.
PD
XX
XX 01-SEP-1998; 98WO-US18084.
PF
XX
XX 02-SEP-1997; 97US-0923771.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX
XX Chen D, Srivatsa GS;
PI
XX
XX WPI; 1999-205198/17.
DR
XX
XX New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
XX
XX Example 9; Page 150; 163pp; English.
PS
XX
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAV23546-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacccttctaccgcgt 17
|||||
Db 1 gacccttctaccgcgt 17

RESULT 4

AAV28169 standard; DNA; 17 BP.

AAV28169;

10-MAY-1999 (first entry)

Target bcl-2 antisense oligonucleotide #29.

Cellular adhesion protein; proliferation; antisense oligonucleotide;
alimentary canal; transport; gastrointestinal mucosa; cancer;
Alzheimer's disease; beta-thalassemia; malaria; viral infection;
HIV; inflammation; ss.

Synthetic.

WO9901579-A1.

14-JAN-1999.

01-JUL-1998; 98WO-US13574.

01-JUL-1997; 97US-0886829.

(ISIS-) ISIS PHARM INC.

Hardee G, Teng C;

WPI: 1999-106077/09.

Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bioavailability

Example 2; Page 85; 11pp; English.

A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAV28169 to AAV18799 and AAV18801 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention.

Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 6.9; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacccttctaccgcgt 17
|||||
Db 1 gacccttctaccgcgt 17

RESULT 5

AAQ86643 standard; DNA; 20 BP.

AAQ86643;

27-SEP-1995 (first entry)

Antisense oligomer TI-AS.

Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
ss.

Synthetic.

Location/Qualifiers

Key 1:20
FT misc_feature
FT /tag- a
FT /note- "3'-5' (antisense) sequence"

WO9508350-A.

30-MAR-1995.

20-SEP-1994; 94WO-US10725.

20-SEP-1993; 93US-0124256.

(REED/) REED J C.

Reed JC;

WPI: 1995-139394/18.

Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer

Disclosure; Page 13; 108pp; English.

The antisense oligonucleotide TI-AS straddles the translation-initiation site in the mRNA coding strand of the human bcl-2 gene and is complementary to this region. It reduces the expression of bcl-2 gene product thereby inducing programmed cell death of certain cancer cells.

Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 16; Length 20;

Best Local Similarity 100.0%; Pred. No. 83; Mismatches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 cccttctaccgcgt 17
|||||
Db 1 cccttctaccgcgt 15

RESULT 6

AAV28169 standard; DNA; 20 BP.

AAV28169;

08-OCT-1998 (first entry)

Antisense oligonucleotide to bcl-2 mRNA.

Purification; oligonucleotide; matrix; affinity unit;
affinity purification; antisense; bcl-2; ss.

Synthetic.

XX PN WO9827425-A1.
 XX PD 25-JUN-1998.
 XX PF 18-DEC-1997; 97WO-US23284.
 XX PR 19-DEC-1996; 96US-0769951.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Chen D, Cole DL, Srivatsa GS;
 XX DR WPI, 1998-362922/31.
 XX PT Matrix for selective separation of oligonucleotide - useful for,
 XX PT e.g. large scale purification of anti-sense agents from their
 XX PT deletion derivatives formed during synthesis
 XX PS Disclosure; Page 76; 183pp; English.
 XX CC AAV28155-268 represent oligonucleotides which can be purified using the
 XX CC method of the invention. The specification describes a matrix that
 XX CC comprises a support and an affinity unit that specifically and
 XX CC reversibly binds a target oligonucleotide, and comprises a sequence of
 XX CC bases having the reverse complement of a hybridizing portion of the
 XX CC target oligonucleotide. The matrix is used for affinity purification of
 XX CC synthetic oligonucleotides, specifically antisense agents, for treatment
 XX CC of hyperproliferative diseases, for treating a non-pathogen,
 XX CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 XX CC expression of cell surface proteins, and to inhibit a eukaryotic
 XX CC pathogen, retrovirus or other viruses.
 XX SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 19; Length 20;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cccctcctaccgcgt 17
 |||||
 Db 1 cccctcctaccgcgt 15

RESULT 7
 AAX23681
 ID AAX23681 standard; DNA; 20 BP.
 XX AC AAX23681;
 XX DT 18-JUN-1999 (first entry)
 XX DE Deletion sequence oligonucleotide 134.
 XX KW Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
 KW probe; cellular adhesion modulator; cellular proliferation modulator;
 KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
 KW HIV; primer; ss.
 XX OS Synthetic.
 XX PN WO9911820-A1.
 XX PD 11-MAR-1999.
 XX PF 01-SEP-1998; 98WO-US18084.
 XX PR 02-SEP-1997; 97US-0923771.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Chen D, Srivatsa GS;

XX DR WPI, 1999-205198/17.
 XX PT New compositions comprising sensor arrays made up of unique probe
 XX PT oligonucleotides - useful for characterizing a sample of target
 XX PT deletion oligonucleotides
 XX PS Example 9; Page 147; 163pp; English.
 XX CC This invention describes a novel composition comprising a number of
 XX CC sensor arrays, where each array comprises a unique probe
 XX CC oligonucleotide, which is the reverse complement of part of a unique
 XX CC target oligonucleotide present in a mixture of target deletion sequence
 XX CC oligonucleotides. The compositions form a method for characterizing a
 XX CC sample of target deletion oligonucleotides which are labeled and
 XX CC hybridize with the probe oligonucleotides of the sensor arrays. Such
 XX CC oligonucleotides and their targets are represented in AAX23548-X23709.
 XX CC Oligonucleotides characterized by the method form pharmaceutical
 XX CC compositions that are useful for modulating cellular adhesion or
 XX CC proliferation, and being active against a eukaryotic pathogen, a human
 XX CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
 XX CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
 XX CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
 XX CC characterization of deletion sequence oligonucleotides having related,
 XX CC but different nucleobase sequences, and quantification of different
 XX CC species of deletion sequence ("target") oligonucleotides in a mixture.
 XX CC Also, if the specificity of the oligonucleotide's nucleobase sequence
 XX CC for its reverse complement is not modified, the method may be performed
 XX CC using oligodeoxynucleotides.
 XX SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cccctcctaccgcgt 17
 |||||
 Db 1 cccctcctaccgcgt 15

RESULT 8
 AAX18690
 ID AAX18690 standard; DNA; 20 BP.
 XX AC AAX18690;
 XX DT 10-MAR-1999 (first entry)
 XX DE Target bcl-2 antisense oligonucleotide #22.
 XX KW Cellular adhesion protein; proliferation; antisense oligonucleotide;
 KW alimentary canal; transport; gastrointestinal mucosa; cancer;
 KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
 KW HIV; inflammation; ss.
 XX OS Synthetic.
 XX PN WO9901579-A1.
 XX PD 14-JAN-1999.
 XX PF 01-JUL-1998; 98WO-US13574.
 XX PR 01-JUL-1997; 97US-0886829.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Hardee G, Teng C;
 XX DR WPI, 1999-106077/09.

PT Composition comprising nucleic acid and penetration enhancer - used
 PT particularly for delivering therapeutic antisense oligonucleotides
 PT across the gastrointestinal mucosa, provides high bioavailability
 XX
 PS Example 2; Page 83; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a
 CC nucleic acid and at least one penetration enhancer. The compositions are
 CC used: (i) to treat or prevent any disease or disorder that can be
 CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
 CC beta-thalassemia, malaria, viral infections (including human immune
 CC deficiency virus (HIV)), inflammation, in human or animal medicine;
 CC (ii) to investigate the role of a gene or gene product in non-human
 CC animals; and (iii) to modulate gene expression in cells, tissues or
 CC organs. The compositions provide bioavailability of at least 15,
 CC preferably 17-35,%. The penetration enhancer improves: (i) transport of
 CC the nucleic acid across the mucosa of the alimentary canal and into
 CC cells; and (ii) increases stability of the nucleic acid. Oral
 CC administration avoids the complications and expense of intravenous or
 CC other methods of administration. AA418669 to AA418799 and AA418801
 CC represent antisense oligonucleotides which can be used as the nucleic
 CC acid in the method of the invention.
 CC
 XX

SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 20; Length 20;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cccctcctaccgcgt 17
 |||
 Db 1 cccctcctaccgcgt 15

RESULT 9

AA49348

ID AA49348 standard; DNA; 20 BP.

AC AA49348;

DT 14-MAR-2000 (first entry)

DE bcl-2 targeted antisense oligonucleotide SEQ ID 13.

KW Cellular proliferation; expression; modulation; antisense;

KW non-parenteral; delivery; uptake; administration; emulsion;

KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;

ss.

OS Synthetic.

OS Homo sapiens.

PN WO960012-A1.

PD 25-NOV-1999.

PF 20-MAY-1999; 99WO-US11394.

PR 21-MAY-1998; 98US-0082624.

PA (ISIS-) ISIS PHARM INC.

PI Teng C, Cook PD, Tillman L, Hardee GE, Ecker DJ, Manoharan M;

DR WPI: 2000-072428/06.

XX New oligonucleotide compositions used for the non-parenteral delivery

PT of e.g. antisense oligos, ribozymes, peptide nucleic acids, molecular

PT decoys, external guide sequences or aptamers

XX Example 2; Page 122; 133pp; English.

CC Sequences AA49344-249354, AA49384-249385, AA49387-249388 and
 CC AA49392-24993 represent antisense oligonucleotides designed
 CC to modulate the rate of cellular proliferation. The invention relates to
 CC new compositions for the non-parenteral delivery of oligonucleotides
 CC comprising at least one oligonucleotide in an emulsion. Oligonucleotides
 CC delivered via the compositions of the invention can be used to modulate
 CC expression of a cellular adhesion protein, modulate a rate of cellular
 CC proliferation, or have biological activity against eukaryotic pathogens
 CC or retroviruses. They can be used for treating conditions including
 CC e.g., ulcerative colitis, Crohn's disease, inflammatory bowel disease
 CC or undue cellular proliferation. The compositions can enhance the local
 CC and systemic uptake and delivery of nucleic acids via non-parenteral
 CC routes of administration (e.g., via the alimentary canal, skin, eyes,
 CC pulmonary tract, urethra or vagina).
 XX

SQ Sequence 20 BP; 2 A; 10 C; 4 G; 4 T; 0 other;

Query Match 88.2%; Score 15; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 83;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cccctcctaccgcgt 17
 |||
 Db 1 cccctcctaccgcgt 15

RESULT 10

AA086653

ID AA086653 standard; DNA; 17 BP.

AC AA086653;

DT 27-SEP-1995 (first entry)

DE bcl-2 antisense oligonucleotide.

KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW lymphoma; programmed cell death; ss.

OS Synthetic.

FH Key Location/Qualifiers

FT misc_feature 1..17

FT /tag= "a"

FT /note= "3'-5' (antisense) sequence"

PN WO9508350-A.

PD 30-MAR-1995.

PF 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI: 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment

PT of human solid tumours, esp. breast cancer

XX Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce

CC programmed cell death (DNA fragmentation) in the human lymphoma cell

CC line RS1846. The oligonucleotides are phosphodiester targeted

CC against the translation initiation site (AA086650-55) or the 5'-cap

CC region (AA086656-58) of human bcl-2 pre-mRNA.

XX

SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ccttcctaccgct 17
 |||||
 DB 1 ccttcctaccgct 14

RESULT 11

AAQ86655 standard; DNA; 17 BP.

AC AAQ86655;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

KM Anticore oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
 LYmphoma; programmed cell death; ss.

OS Synthetic.

FT Key Location/Qualifiers
 FT misc-feature 1..17
 /tag= a
 /note= "3'-5' (antisense) sequence"

WO9508350-A.

30-MAR-1995.

PE 20-SEP-1994; 94WO-US10725.

PR 20-SEP-1993; 93US-0124256.

PA (REED/) REED J C.

PI Reed JC;

DR WPI; 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
 PT of human solid tumors, esp. breast cancer
 PS Example 12; Page 33; 108pp; English.

CC Antisense oligonucleotides were tested for their ability to induce
 CC programmed cell death (DNA fragmentation) in the human lymphoma cell
 CC line RS1846. The oligonucleotides are phosphodiester targets
 CC against the translation initiation site (AAQ86650-55) or the 5'-cap
 CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.

XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gaccctcctaccg 14
 |||||
 DB 4 gaccctcctaccg 17

RESULT 12

AAV28175 standard; DNA; 17 BP.

AC AAV28175;

XX 08-OCT-1998 (first entry)

XX Antisense oligonucleotide to bcl-2 mRNA.

DE Purification; oligonucleotide; matrix; affinity unit;
 XX affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

XX 25-JUN-1998.

PD 18-DEC-1997; 97WO-US23284.

PR 19-DEC-1996; 96US-0769951.

PA (ISIS-) ISIS PHARM INC.

XX Chen D, Cole DL, Srivatsa GS;

PI WPI; 1998-362922/31.

XX Matrix for selective separation of oligonucleotide - useful for,
 PT e.g. large scale purification of anti-sense agents from their
 PT deletion derivatives formed during synthesis

PS Disclosure; Page 81; 183pp; English.

XX AAQ86655-268 represent oligonucleotides which can be purified using the
 CC method of the invention. The specification describes a matrix that
 CC comprises a support and an affinity unit that specifically and
 CC reversibly binds a target oligonucleotide, and comprises a sequence of
 CC bases having the reverse complement of a hybridizing portion of the
 CC target oligonucleotide. The matrix is used for affinity purification of
 CC synthetic oligonucleotides, specifically antisense agents, for treatment
 CC of hyperproliferative diseases, for treating a non-pathogen,
 CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
 CC expression of cell surface proteins, and to inhibit a eukaryotic
 CC pathogen, retrovirus or other viruses.

XX Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ccttcctaccgct 17
 |||||
 DB 1 ccttcctaccgct 14

RESULT 13

AAV28177 standard; DNA; 17 BP.

AC AAV28177;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

XX Purification; oligonucleotide; matrix; affinity unit;
 KM affinity purification; antisense; bcl-2; ss.

OS Synthetic.

PN WO9827425-A1.

XX 25-JUN-1998.

PF 18-DEC-1997; 97WO-US23284.
XX
PR 19-DEC-1996; 96US-0769951.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Cole DL, Srivatsa GS;
XX
DR WPI; 1998-362922/31.
XX
PT Matrix for selective separation of oligo:nucleotide - useful for,
PR e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
PS Disclosure; Page 83; 183pp; English.
XX
CC AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgcg 14
Db 4 gaccctctaccgcg 17

RESULT 14
AA23687
ID AAX23687 standard; DNA; 17 BP.
XX
AC AAX23687;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 140.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target

PT deletion oligonucleotides
XX
XX Example 9; Page 150; 163pp; English.
PS
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23348-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC syncytial virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ccttctaccgcgcgt 17
Db 1 ccttctaccgcgcgt 14

RESULT 15
AAX23689
ID AAX23689 standard; DNA; 17 BP.
XX
AC AAX23689;
XX
DT 18-JUN-1999 (first entry)
XX
DE Deletion sequence oligonucleotide 142.
XX
KM Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KM probe; cellular adhesion modulator; cellular proliferation modulator;
KM human retrovirus; human immunodeficiency virus; non-human retrovirus;
KM HIV; primer; ss.
XX
OS Synthetic.
XX
PN WO9911820-A1.
PD 11-MAR-1999.
XX
PF 01-SEP-1998; 98WO-US18084.
XX
PR 02-SEP-1997; 97US-0923771.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Chen D, Srivatsa GS;
XX
DR WPI; 1999-205198/17.
XX
PT New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
PS Example 9; Page 151; 163pp; English.

XX This invention describes a novel composition comprising a number of
 CC sensor arrays, where each array comprises a unique probe
 CC oligonucleotide, which is the reverse complement of part of a unique
 CC target oligonucleotide present in a mixture of target deletion sequence
 CC oligonucleotides. The compositions form a method for characterizing a
 CC sample of target deletion oligonucleotides which are labeled and
 CC hybridize with the probe oligonucleotides of the sensor arrays. Such
 CC oligonucleotides and their targets are represented in AAX23548-X23709.
 CC Oligonucleotides characterized by the method form pharmaceutical
 CC compositions that are useful for modulating cellular adhesion or
 CC proliferation, and being active against a eukaryotic pathogen, a human
 CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
 CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
 CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
 CC characterization of deletion sequence oligonucleotides having related,
 CC but different nucleobase sequences, and quantification of different
 CC species of deletion sequence ("target") oligonucleotides in a mixture.
 CC Also, if the specificity of the oligonucleotide's nucleobase sequence
 CC for its reverse complement is not modified, the method may be performed
 CC using oligodeoxynucleotides.

XX
 SQ Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gacccttctaccg 14
 |||||
 Db 4 gacccttctaccg 17

Search completed: June 28, 2002, 22:40:15
 Job time: 8091 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:48 ; Search time 334.55 Seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-12

Perfect score: 17

Sequence: 1 gacccctcaccgcgt 17

Scoring table: IDENTITY NUC

Searched: Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	100.0	17	2	US-08-465-485A-12
2	17	100.0	17	3	US-09-080-285-12
3	14	82.4	17	2	US-08-465-485A-11
4	14	82.4	17	2	US-08-465-485A-13
5	14	82.4	17	3	US-09-080-285-13
6	14	82.4	17	3	US-09-080-285-13
7	12.4	72.9	40	1	US-08-231-342-17
8	12.2	71.8	67	2	US-08-477-527A-44
9	12.2	71.8	67	3	US-08-481-710-44
10	12.2	71.8	67	5	PCT-US96-0937-44
11	11.8	69.4	30	1	US-08-384-708A-143
12	11.8	69.4	30	1	US-08-384-708A-147
13	11.8	69.4	30	4	US-08-687-421-143
14	11.8	69.4	30	4	US-08-687-421-147
15	11.4	67.1	28	4	US-08-870-930-56
16	11.4	67.1	28	4	US-08-870-930-57
17	11.4	67.1	29	4	US-08-870-930-74
18	11.4	67.1	29	4	US-08-870-930-75
19	11.4	67.1	29	4	US-08-870-930-76
20	11.4	67.1	29	4	US-08-870-930-77
21	11.4	67.1	30	4	US-08-870-930-55
22	11.4	67.1	32	2	US-08-305-764C-21
23	11.4	67.1	55	4	US-08-531-025-5
24	11.4	67.1	61	4	US-08-870-930-17
25	11.4	67.1	61	4	US-08-870-930-22
26	11.4	67.1	61	4	US-09-275-850-56
27	11.2	65.9	26	1	US-08-318-193-28

28	11.2	65.9	26	1	US-08-318-193-29	Sequence 29, Appl
29	11.2	65.9	30	1	US-08-236-311-14	Sequence 14, Appl
30	11.2	65.9	50	3	US-08-457-918-14	Sequence 14, Appl
31	11.2	65.9	52	6	5200327-11	Patent No. 5200327
32	11.2	65.9	60	1	US-08-484-192-154	Sequence 154, App
33	11.2	65.9	70	2	US-08-894-578-138	Sequence 138, App
34	11	64.7	17	2	US-08-465-485A-10	Sequence 10, Appl
35	11	64.7	17	3	US-09-080-285-10	Sequence 10, Appl
36	11	64.7	23	4	US-08-870-930-58	Sequence 58, Appl
37	11	64.7	23	4	US-08-870-930-84	Sequence 84, Appl
38	11	64.7	57	3	US-09-135-639-9	Sequence 9, Appl
39	11	64.7	57	3	US-09-135-639-9	Sequence 9, Appl
40	11	64.7	60	4	US-09-339-913B-26	Sequence 26, Appl
41	11	64.7	60	4	US-09-339-904A-26	Sequence 26, Appl
42	11	64.7	60	4	US-08-769-062B-26	Sequence 26, Appl
43	11	64.7	60	4	US-09-344-002B-26	Sequence 26, Appl
44	10.8	63.5	24	3	US-08-744-590-1	Sequence 1, Appl
45	10.8	63.5	24	3	US-09-160-671-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-465-485A-12
Sequence 12, Application US/08465485A
Patent No. 5631066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-12

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
|||||
Db 1 GACCTTCTACCGCGT 17

RESULT 2

US-09-080-285-12
; Sequence 12, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-12

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
|||||
Db 1 GACCTTCTACCGCGT 17

RESULT 3
US-08-465-485A-11
; Sequence 11, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-11

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ccttctaccgcgt 17
|||||
Db 1 CCTTCTACCGCGT 14

RESULT 4
US-08-465-485A-13
; Sequence 13, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-11

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-08-465-485A-13

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0;

QY 1 gaccctctaccg 14
DB 4 GACCCTCTACCG 17

RESULT 5
US-09-080-285-11
Sequence 11, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-11

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0;

QY 4 cctctaccgcgt 17
DB 1 CCTCTACCGCGT 14

RESULT 6
US-09-080-285-13
Sequence 13, Application US/09080285
Patent No. 6040181
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-13

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gaccctctcaccg 14
|||||
Db 4 GACCCCTCTACCG 17

RESULT 7
US-08-231-342-17/c
Sequence 17, Application US/08211342
Patent No. 5827684
GENERAL INFORMATION:
APPLICANT: Sreekishna, Kotikanyadanam
APPLICANT: Prevatt, William D
APPLICANT: Thill, Gregory P
APPLICANT: Davila, Geneva R
APPLICANT: Koulitz, Patricia
APPLICANT: Barr, Kathryn A
APPLICANT: Hopkins, Sharon A
TITLE OF INVENTION: Production of Bacillus Entomotoxins in
TITLE OF INVENTION: Methyloctrophic Yeast
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603-4277
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,342
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/926,448
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REGISTRATION NUMBER: 33,129
REFERENCE/DOCKET NUMBER: 52627
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842

TELEFAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-231-342-17

Query Match 72.9%; Score 12.4; DB 1; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 gaccctctcaccg 14
|||||
Db 40 GACCCCTCTACCG 27

RESULT 8
US-08-477-527A-44/c
Sequence 44, Application US/08477527A
Patent No. 5972599
GENERAL INFORMATION:
APPLICANT: DIANE TASSETT
APPLICANT: NIKOS PAGRADIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-477-527A-44

Query Match 71.8%; Score 12.2; DB 2; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
||||| || |||||
DB 44 GACCCTTACTCTCGCGT 28

RESULT 9
US-08-481-710-44/C
Sequence 44, Application US/08481710
Patent No. 6028186
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,710
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
APPLICATION DATA:
APPLICATION NUMBER: 07/114,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearen
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-2
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-481-710-44

Query Match 71.8%; Score 12.2; DB 3; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gaccctctaccgcgt 17
||||| || |||||
DB 44 GACCCTTACTCTCGCGT 28

RESULT 10
PCT-US96-09537-44/C
Sequence 44, Application PC/TUS9609537
GENERAL INFORMATION:
APPLICANT: NEXSTAR PHARMACEUTICALS, INC.
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09537
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,829
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/481,710
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX41/PCT
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-NH2
US-08-481-710-44

Query Match 71.8%; Score 12.2; DB 5; Length 67;
Best Local Similarity 82.4%; Pred. No. 3.4e+02;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gacccttactacgcgt 17
||||| 11 |||||
Db 44 GACCCTTACTCTCGCGT 28

RESULT 11

US-08-384-708A-143/c

; Sequence 143, Application US/08384708A
; Patent No. 5639868

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; APPLICANT: Janjic, Nedojca

; TITLE OF INVENTION: High-Affinity RNA Ligands of Basic

; TITLE OF INVENTION: Fibroblast Growth Factors

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,708A

; FILING DATE: 02-FEBRUARY-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/195,005

; FILING DATE: 10-FEBRUARY-1994

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/536,428

; FILING DATE: 11-JUNE-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX07/D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 143:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: All C's are 2'-NH2 cytosine

; OTHER INFORMATION: All U's are 2'-NH2 uracil

; US-08-384-708A-143

; Query Match 69.4%; Score 11.8; DB 1; Length 30;

; Best Local Similarity 86.7%; Pred. No. 5.2e+02;

; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acccttactacgcg 16
||||| 11 ||||| 11
Db 27 ACCCATCTACCCCG 13

RESULT 12

US-08-384-708A-147/c

; Sequence 147, Application US/08384708A
; Patent No. 5639868

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; APPLICANT: Janjic, Nedojca

; TITLE OF INVENTION: High-Affinity RNA Ligands of Basic

; TITLE OF INVENTION: Fibroblast Growth Factors

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Swanson & Bratschun, L.L.C.

; STREET: 8400 E. Prentice Avenue, Suite 200

; CITY: Englewood

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage

; COMPUTER: IBM compatible

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/384,708A

; FILING DATE: 02-FEBRUARY-1995

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/195,005

; FILING DATE: 10-FEBRUARY-1994

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/714,131

; FILING DATE: 10-JUNE-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Barry J. Swanson

; REGISTRATION NUMBER: 33,215

; REFERENCE/DOCKET NUMBER: NEX07/D

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (303) 793-3333

; TELEFAX: (303) 793-3433

; INFORMATION FOR SEQ ID NO: 147:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 30 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: All C's are 2'-NH2 cytosine

; OTHER INFORMATION: All U's are 2'-NH2 uracil

; US-08-384-708A-147

; Query Match 69.4%; Score 11.8; DB 1; Length 30;

; Best Local Similarity 86.7%; Pred. No. 5.2e+02;

; Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 acccttactacgcg 16
||||| 11 ||||| 11
Db 27 ACCCATCTACCCCG 13

RESULT 13

US-08-687-421-143/c

; Sequence 143, Application US/08687421

; Patent No. 6177557

; GENERAL INFORMATION:

; APPLICANT: Gold, Larry

; APPLICANT: Janjic, Nedojca

; APPLICANT: Tasset, Diane

; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC

TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-687-421-143

Query Match 69.4%; Score 11.8; DB 4; Length 30;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctctacgcgcg 16
||||| ||||| |||
DB 27 ACCCATCCTACCCCG 13

RESULT 14
US-08-687-421-147/C
Sequence 147, Application US/08687421
Patent No. 6177557
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa

APPLICANT: Tassel, Diane
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: All C's are 2'-NH2 cytosine
FEATURE:
OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-687-421-147

Query Match 69.4%; Score 11.8; DB 4; Length 30;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 accctctacgcgcg 16
||||| ||||| |||
DB 27 ACCCATCCTACCCCG 13

RESULT 15
US-08-870-930-56/C
Sequence 56, Application US/08870930
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa

APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VARGESE, MICHAEL
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,930
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ. ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
US-08-870-930-56

Query Match 67.1%; Score 11.4; DB 4; Length 28;
Best Local Similarity 92.3%; Pred. No. 8.5e+02;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 cttctactacgcgt 17
|||||||
Db 17 CTTCTACTACGCAT 5

Search completed: June 28, 2002, 22:16:49
Job time: 8275 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:11 ; Search time 3762.88 Seconds
(without alignments)
94.542 Million cell updates/sec

Title: US-09-709-170A-13
Perfect score: 17
Sequence: 1 ggagaccctctctaccg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_scs:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlgo_inv:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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1	17	100.0	17	6	AR052615	AR052615 Sequence
2	14	82.4	17	6	AR052614	AR052614 Sequence
3	13.8	81.2	72	9 <th>HUMTCGDPB</th> <th>M28772 Human T-cell</th>	HUMTCGDPB	M28772 Human T-cell
4	13.4	78.8	47	9 <th>HUMTCVD1BQ</th> <th>I32414 Human T-cell</th>	HUMTCVD1BQ	I32414 Human T-cell
5	12.8	75.3	45	6 <th>A50066</th> <th>A50066 Sequence 18</th>	A50066	A50066 Sequence 18
6	12.8	75.3	45	6 <th>AR083363</th> <th>AR083363 Sequence</th>	AR083363	AR083363 Sequence
7	12.8	75.3	47	9 <th>HUMTCVJ32</th> <th>I39499 Homo sapien</th>	HUMTCVJ32	I39499 Homo sapien
8	12.8	75.3	51	6 <th>AX204517</th> <th>AX204517 Sequence</th>	AX204517	AX204517 Sequence
9	12.4	72.9	18	6 <th>AX119389</th> <th>AX119389 Sequence</th>	AX119389	AX119389 Sequence
10	12.4	72.9	20	6 <th>BD009422</th> <th>BD009422 Probes, m</th>	BD009422	BD009422 Probes, m
11	12.4	72.9	40	6 <th>AR050327</th> <th>BD009422 Sequence</th>	AR050327	BD009422 Sequence
12	12.2	71.8	53	9 <th>HUMTCVD1DN</th> <th>I32463 Human T-cell</th>	HUMTCVD1DN	I32463 Human T-cell
13	12.2	71.8	59	9 <th>HUMTCRAD2</th> <th>I39615 Homo sapien</th>	HUMTCRAD2	I39615 Homo sapien
14	12.2	71.8	71	6 <th>AR092263</th> <th>AR172707 Sequence</th>	AR092263	AR172707 Sequence
15	12	70.6	60	6 <th>AR172707</th> <th>AR172707 Sequence</th>	AR172707	AR172707 Sequence
16	11.8	69.4	18	6 <th>A52768</th> <th>A52768 Sequence 12</th>	A52768	A52768 Sequence 12
17	11.8	69.4	18	6 <th>AR137982</th> <th>AR137982 Sequence</th>	AR137982	AR137982 Sequence
18	11.8	69.4	18	6 <th>AX138682</th> <th>AX138682 Sequence</th>	AX138682	AX138682 Sequence
19	11.8	69.4	19	6 <th>AR097399</th> <th>AR097399 Sequence</th>	AR097399	AR097399 Sequence
20	11.8	69.4	19	6 <th>I25704</th> <th>I25704 Sequence 23</th>	I25704	I25704 Sequence 23
21	11.8	69.4	60	6 <th>AR068207</th> <th>AR068207 Sequence</th>	AR068207	AR068207 Sequence
22	11.8	69.4	60	6 <th>AR076959</th> <th>AR076959 Sequence</th>	AR076959	AR076959 Sequence
23	11.8	69.4	60	6 <th>AR078792</th> <th>AR078792 Sequence</th>	AR078792	AR078792 Sequence
24	11.8	69.4	71	6 <th>I05090</th> <th>I05090 Sequence 1</th>	I05090	I05090 Sequence 1
25	11.8	69.4	74	6 <th>AR147504</th> <th>AR147504 Sequence</th>	AR147504	AR147504 Sequence
26	11.4	67.1	18	6 <th>AX098738</th> <th>AX098738 Sequence</th>	AX098738	AX098738 Sequence
27	11.4	67.1	20	6 <th>E03458</th> <th>E03458 Oligo DNA P</th>	E03458	E03458 Oligo DNA P
28	11.4	67.1	20	6 <th>E03451</th> <th>E03451 Oligonucleo</th>	E03451	E03451 Oligonucleo
29	11.4	67.1	26	6 <th>AR089980</th> <th>AR089980 Sequence</th>	AR089980	AR089980 Sequence
30	11.4	67.1	28	6 <th>AX283122</th> <th>AX283122 Sequence</th>	AX283122	AX283122 Sequence
31	11.4	67.1	28	6 <th>AX283124</th> <th>AX283124 Sequence</th>	AX283124	AX283124 Sequence
32	11.4	67.1	32	6 <th>AR026317</th> <th>AR026317 Sequence</th>	AR026317	AR026317 Sequence
33	11.4	67.1	48	6 <th>AX201571</th> <th>AX201571 Sequence</th>	AX201571	AX201571 Sequence
34	11.4	67.1	50	6 <th>AX164949</th> <th>AX164949 Sequence</th>	AX164949	AX164949 Sequence
35	11.4	67.1	51	6 <th>AX204129</th> <th>AX204129 Sequence</th>	AX204129	AX204129 Sequence
36	11.4	67.1	51	6 <th>AX204257</th> <th>AX204257 Sequence</th>	AX204257	AX204257 Sequence
37	11.4	67.1	55	6 <th>AR172872</th> <th>AR172872 Sequence</th>	AR172872	AR172872 Sequence
38	11.4	67.1	55	6 <th>AX057560</th> <th>AX057560 Sequence</th>	AX057560	AX057560 Sequence
39	11.4	67.1	60	10 <th>AF265815</th> <th>AF265815 Mus muscu</th>	AF265815	AF265815 Mus muscu
40	11.4	67.1	62	6 <th>AX193276</th> <th>AX193276 Sequence</th>	AX193276	AX193276 Sequence
41	11.4	67.1	62	6 <th>AX193441</th> <th>AX193441 Sequence</th>	AX193441	AX193441 Sequence
42	11.4	67.1	67	6 <th>AX193327</th> <th>AX193327 Sequence</th>	AX193327	AX193327 Sequence
43	11.4	67.1	67	6 <th>AX193345</th> <th>AX193345 Sequence</th>	AX193345	AX193345 Sequence
44	11.4	67.1	68	6 <th>A41650</th> <th>A41650 Sequence 7</th>	A41650	A41650 Sequence 7
45	11.4	67.1	68	6 <th>A73712</th> <th>A73712 Sequence 5</th>	A73712	A73712 Sequence 5

ALIGNMENTS

RESULT 1	AR052615	AR052615	17 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR052615	Sequence 13 from patent US 5831066.				
DEFINITION	AR052615					
ACCESSION	AR052615.1	GI:5975979				
VERSION						
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 17)					
AUTHORS	Reed J.C.					
TITLE	Regulation of bcl-2 gene expression					
JOURNAL	Patent: US 5831066-A 13 03-NOV-1998;					
FEATURES	Location/Qualifiers					
source	1..17					

BASE COUNT	3 a	7 c	4 g	3 t
ORIGIN				

Query Match	100.0%;	Score 17;	DB 6;	length 17;
Best Local Similarity	100.0%;	Pred. No. 25;		

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagaccctcctaccg 17
Db 1 GGAGACCCCTCCTACCG 17

RESULT 2

AR052614

LOCUS AR052614 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5831066.
ACCESSION AR052614
VERSION AR052614.1 GI:5975978
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

1 (bases 1 to 17)
Reed, J.C.
Regulation of bcl-2 gene expression
Patent: US 5831066-A 12 03-NOV-1998;
Location/Qualifiers

SOURCE

1. 17
/organism="unknown"
BASE COUNT 2 a 8 c 3 g 4 t
ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gaccctcctaccg 17
Db 1 GACCCCTCCTACCG 14

RESULT 3

HMTGCD2B

LOCUS HMTGCD2B 72 bp DNA linear PRI 03-AUG-1993
DEFINITION Human T-cell receptor trans-rearranged gamma-delta-chain gene
V-gamma-D-delta-J-delta region, clone gd2.2.
ACCESSION M28772.1 GI:339093
VERSION M28772
KEYWORDS

D-region; J-region; N-region; T-cell receptor; T-cell receptor
delta chain; T-cell receptor gamma chain; V-region; antigen
receptor; processed gene.
Human thymus DNA, clone gd2.2.
SOURCE

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE

AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES

1 (bases 1 to 72)
Tycko, B., Palmer, J. and Sklar, J.
T cell receptor gene trans-rearrangements: Chimeric gamma-delta
genes in normal lymphoid tissues
Science 245, 1242-1246 (1989)
89388234
Location/Qualifiers

SOURCE

1. 72
/organism="Homo sapiens"
/db_xref="taxon:9606"
<1. >72
/note="T-cell receptor gamma-delta-chain V-D-J-region"
/codon_start=3
/protein_id="AAA36693.1"
/db_xref="GI:553708"
/translation="CATWEPPLPTARGMFCYDKLIFGK"
BASE COUNT 15 a 20 c 18 g 19 t
ORIGIN

Query Match 81.2%; Score 13.8; DB 9; Length 72;
Best Local Similarity 88.2%; Pred. No. 2.2e+03;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctcctaccg 17
Db 14 GGAGACCCCTCCTACTG 30

RESULT 4

HMTGCD1BQ

LOCUS HMTGCD1BQ 47 bp mRNA linear PRI 10-FEB-1995
DEFINITION Human (clone: 1stip131) T-cell receptor delta-chain (V-delta-1)
mRNA.
ACCESSION L32414
VERSION L32414.1 GI:497484
KEYWORDS
SOURCE

T-cell receptor; delta chain.
Homo sapiens intestine cDNA to mRNA.
Homo sapiens
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES

1 (bases 1 to 47)
Kagnoff, M.F., Holtmeier, W., Harwood, J., Morzycka-Wroblewska, E. and
The V delta 1 T cell receptor repertoire in human small intestine
and colon
J. Exp. Med. 180 (1), 183-190 (1994)
94275371
Location/Qualifiers

SOURCE

1. 47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="intestine"
BASE COUNT 10 a 15 c 12 g 10 t
ORIGIN

Query Match 78.8%; Score 13.4; DB 9; Length 47;
Best Local Similarity 93.3%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggagaccctcctacc 15
Db 6 GGAGACCCCTCCTAC 20

RESULT 5

A50066

LOCUS A50066 45 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 18 from Patent WO9612810.
ACCESSION A50066
VERSION A50066.1 GI:2303244
KEYWORDS

unidentified.
unidentified
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

1 (bases 1 to 45)
Lathe, R., Rose, K.A. and Stapleton, G.
HIPPOCAMPUS-ASSOCIATED PROTEINS, DNA SEQUENCES CODING THEREFOR AND
USING THEREFOR
Patent: WO 9612810-A 18 02-MAY-1996;
UNIV EDINBURGH (GB)
Other publication AU 3670395 960515.
Location/Qualifiers

SOURCE

1. 45
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 12 a 15 c 5 g 13 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 45;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctacc 16
|||||
Db 22 GGAGTCCCTCTACC 37

RESULT 6
LOCUS AR083363 45 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 17 from patent US 5976850.
ACCESSION AR083363
VERSION AR083363.1 GI:10010153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Lathé, R., Rose, R. Andrew and Stapleton, G.
TITLE Hippocampus-associated proteins; DNA sequences coding therefor and uses thereof
JOURNAL Patent: US 5976850-A 17 02-NOV-1999;
FEATURES
source location/Qualifiers
BASE COUNT 12 a 15 c 5 g 13 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 45;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ggagaccctctacc 16
|||||
Db 22 GGAGTCCCTCTACC 37

RESULT 7
LOCUS HUMTCCVJ32 47 bp mRNA linear PRI 19-AUG-1995
DEFINITION Homo sapiens (C.2.PL252) rearranged T-cell receptor delta chain (TCRDV2J1) mRNA, partial V-region.
ACCESSION L39499
VERSION L39499.1 GI:945251
KEYWORDS CDR3 region; T-cell receptor alpha-chain; T-cell receptor delta; antigen recognition site; junctional region; rearranged; variable region.
SOURCE Homo sapiens (clone: C.2.PL252) colon cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 47)
AUTHORS Holtmeier, W., Chowers, Y., Lumeng, A., Morzycka-Wroblewska, E. and Kagnoff, M.F.
TITLE The delta T cell receptor repertoire in human colon and peripheral blood is oligoclonal irrespective of V region usage
JOURNAL J. Clin. Invest. 96 (2), 1108-1117 (1995)
MEDLINE 95362812
COMMENT Citation paper.
FEATURES
source location/Qualifiers
1. 47
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="C.2.PL252"
/tissue_type="colon"
<1..>47
/gene="TCRDV2J1"
/standard_name="(V delta-2/J delta-1)"
/note="putative"
1..47
/gene="TCRDV2J1"
/gene="TCRDV2J1"
/note="This CDS feature is included to show the

translation of the corresponding V-region. Presently translation qualifiers on V-region features are illegal."
/codon_start=1
/protein_id="AAC41800.1"
/db_xref="GI:950449"
/translation="ACDRLPTALPNAYKL"
BASE COUNT 12 a 19 c 6 g 10 t
ORIGIN

Query Match 75.3%; Score 12.8; DB 9; Length 47;
Best Local Similarity 87.5%; Pred. No. 9.3e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 ggagaccctctaccg 17
|||||
Db 7 GGAGTCCCTCTACC 22

RESULT 8
LOCUS AX204517 51 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 623 from Patent WO0148245.
ACCESSION AX204517
VERSION AX204517.1 GI:15394084
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 51)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0148245-A 623 05-JUL-2001;
CURRGEN Curagen Corporation (US)
FEATURES
source location/Qualifiers
1. 51
/organism="Homo sapiens"
/db_xref="taxon:9606"
26
/note="single nucleotide polymorphism
Accession number C943970982"
BASE COUNT 13 a 14 c 17 g 7 t
ORIGIN

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Best Local Similarity 87.5%; Pred. No. 9.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ggagaccctctacc 16
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Db 25 GGAGTCCCTCTACC 40

RESULT 9
LOCUS AX119389 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 46 from Patent WO0129251.
ACCESSION AX119389
VERSION AX119389.1 GI:14036308
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Messiaen, L. and Callens, T.
TITLE Improved mutation analysis of the nfi gene
JOURNAL Patent: WO 0129251-A 46 26-APR-2001;
UNIVERSITEIT GENT (BE)
FEATURES
location/Qualifiers

source 1.18
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 3 a 6 c 3 g 6 t
ORIGIN

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Best Local Similarity 92.9%; Pred. No. 1.8e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gagagaccctccta 14
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Db 4 GGTGACCTCCTCA 17

RESULT 10
BD009422 20 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples.
ACCESSION BD009422
VERSION BD009422.1 GI:18637795
KEYWORDS JP 2001502536-A/14.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Quint,W. and Doorn,L.J.V.
TITLE Probes, methods and kits for detection and typing of Helicobacter
pylori nucleic acids in biological samples
JOURNAL Patent: JP 2001502536-A 14 27-FEB-2001;
COMMENT INNOGENETICS NV,DDL BV
OS Unidentified
PN JP 2001502536-A/14
PD 27-FEB-2001
PF 10-OCT-1997 JP 1998518004
PR 16-OCT-1996 EP 96870131.8
PI WILHELMUS QUINT,LEENDERT JAN VAN DOORN
PC C1201/68,C07K14/205,C12M15/11
CC
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
FEATURES
source 1..20
Location/Qualifiers
BASE COUNT 4 a 8 c 3 g 4 t 1 others
ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 20;
Best Local Similarity 81.2%; Pred. No. 1.8e+04;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 gagagaccctcctacg 17
||| ||||| |||||
Db 4 GARACGCTCTACAG 19

RESULT 11
AR050327 40 bp DNA linear PAT 29-SEP-1995
LOCUS
DEFINITION Sequence 17 from patent US 5827684.
ACCESSION AR050327
VERSION AR050327.1 GI:5973052
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 40)
AUTHORS Steekrisma,K., Prevatt,W.D., Thill,G.P., Davis,G.R., Koutz,P.,

TITLE Barr,K.A. and Hopkins,S.A.
JOURNAL Production of Bacillus entomotoxins in methylotrophic yeast
ORIGIN Patent: US 5827684-A 17 27-OCT-1998;
Location/Qualifiers
source 1..40
/organism="unknown"
BASE COUNT 11 a 8 c 10 g 11 t
ORIGIN

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Best Local Similarity 92.9%; Pred. No. 1.7e+04;
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QY 4 gaccctcctacg 17
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Db 40 GACCGTCTACCG 27

RESULT 12
HUMTCVD1DN 53 bp mRNA linear PRI 10-FEB-1995
LOCUS Human (clone: 3cpj23) T-cell receptor delta-chain (V-delta-1) mRNA.
DEFINITION L32463
ACCESSION L32463.1 GI:497533
VERSION L32463.1 GI:497533
KEYWORDS T-cell receptor; delta chain.
SOURCE Homo sapiens intestine cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 53)
AUTHORS Chowers,Y., Holmeier,W., Harwood,J., Morzycka-Wroblewska,E. and Kagnoff,M.F.
TITLE The V delta 1 T cell receptor repertoire in human small intestine
JOURNAL J. Exp. Med. 180 (1), 183-190 (1994)
MEDLINE 94275371
FEATURES
source 1..53
Location/Qualifiers
BASE COUNT 7 a 15 c 18 g 13 t
ORIGIN

Query Match 71.8%; Score 12.2; DB 9; Length 53;
Best Local Similarity 82.4%; Pred. No. 2.2e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 gagagaccctcctacg 17
||| ||||| |||||
Db 6 GGGGACCACTCTACTG 22

RESULT 13
HUMTCRAD2 59 bp mRNA linear PRI 21-AUG-1995
LOCUS Homo sapiens (C.A.LR02) rearranged T-cell receptor delta chain
DEFINITION (TCRAV1452-TCRDJ1) mRNA, partial V-region.
ACCESSION L39615
VERSION L39615.1 GI:945298
KEYWORDS CDR3 region; T-cell receptor alpha-chain; T-cell receptor delta; antigen recognition site; junctional region; rearranged; variable region.
SOURCE Homo sapiens (clone: C.A.LR02) colon cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 59)
AUTHORS Holmeier,W., Chowers,Y., Lumeng,A., Morzycka-Wroblewska,E. and Kagnoff,M.F.
TITLE The delta T cell receptor repertoire in human colon and peripheral

Mon Jul 1 08:40:48 2002

us-09-709-170a-13.szlm75.rge

GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:40:15 : Search time 1381.16 seconds

(without alignments)
21.133 Million cell updates/sec

Title: US-09-709-170a-13

Perfect score: 17
Sequence: 1 gagagacctctaccg 17

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 1996432

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	AAQ86655	Bcl-2 antisense ol
2	17	100.0	17	AAV28177	Antisense oligonuc
3	17	100.0	17	AAV28177	Deletion sequence
4	17	100.0	17	AAV28177	Target bcl-2 antis
5	14	82.4	17	AAO86654	Bcl-2 antisense ol
6	14	82.4	17	AAV28176	Antisense oligonuc
7	14	82.4	17	AAV28176	Deletion sequence
8	14	82.4	17	AAV28176	Target bcl-2 antis
9	12.8	75.3	17	AAV28176	Hammerhead ribozym

10	12.8	75.3	45	17	AAV28176	Rat clone 13 Hct-1
11	12.8	75.3	51	22	AAH80008	Human DNA containi
12	12.4	72.9	18	22	AAH80008	Neurofibromatosis
13	12.4	72.9	20	19	AAV73521	H. pylori vacA pri
14	12.4	72.9	21	19	AAV26082	Human polymorphic
15	12.2	71.8	17	22	AAV26082	Plasmid B1154 distr
16	12.2	71.8	71	17	AAV7816	Nucleic acid inhib
17	12.2	71.8	71	21	AAV27225	Activated neutroph
18	12.2	71.8	19	17	AAV27370	Anti-ras oncogene
19	12	70.6	20	16	AAO86643	Antisense oligomer
20	12	70.6	20	19	AAV28169	Antisense oligonuc
21	12	70.6	20	20	AAV23681	Deletion sequence
22	12	70.6	20	20	AAV18690	Target bcl-2 antis
23	12	70.6	20	21	AAV43348	bcl-2 targeted an
24	12	70.6	47	21	AAV67538	Human map-related
25	12	70.6	60	19	AAV40205	Escherichia coli B
26	11.8	69.4	17	21	AAV02834	Hammerhead ribozym
27	11.8	69.4	18	17	AAV35217	Murine adenylate c
28	11.8	69.4	19	17	AAV08657	Primer P53-5X2SP0
29	11.8	69.4	19	18	AAV99826	Primer for exon 2
30	11.8	69.4	19	18	AAV99856	Human map-related
31	11.8	69.4	47	21	AAV68232	Human map-related
32	11.8	69.4	50	22	AAV29457	Human SNP oligonuc
33	11.8	69.4	60	17	AAV42991	Fusion junction fo
34	11.8	69.4	71	8	AAV70046	DNA probe specific
35	11.8	69.4	74	22	AAV83238	S. cerevisiae yDR0
36	11.6	68.2	60	21	AAV29520	Codon altered alka
37	11.4	67.1	18	22	AAV01877	Cytochrome P-450 (
38	11.4	67.1	20	13	AAV024088	Primer DNA 9. Syn
39	11.4	67.1	20	13	AAV024112	Primer DNA 8. Syn
40	11.4	67.1	20	20	AAV05149	PCR primer used to
41	11.4	67.1	20	21	AAV05082	Human fir-1 mRNA a
42	11.4	67.1	22	13	AAV02908	HCV-Hc59 primer #7
43	11.4	67.1	22	20	AAV26649	Oligonucleotide us
44	11.4	67.1	28	22	AAV68635	HSPDE41 coding re
45	11.4	67.1	28	22	AAV68637	HSPDE44 DNA fragm

ALIGNMENTS

RESULT 1	
AAQ86655	
ID	AAQ86655 standard; DNA; 17 Bp.
XX	
AC	AAQ86655;
XX	
DT	27-SEP-1995 (first entry)
XX	
DE	Bcl-2 antisense oligonucleotide.
XX	
KW	Anticodon oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW	Lymphoma; programmed cell death; ss.
XX	
OS	Synthetic.
XX	
PH	Key
FT	misc-feature
FT	1..17
FT	Location/Qualifiers
FT	/*tag= a
XX	/note= "3'-5' (antisense) sequence"
PN	W09508350-A.
XX	
PD	30-MAR-1995.
XX	
PF	20-SEP-1994; 94MO-US10725.
XX	
PR	20-SEP-1993; 93US-0124256.
XX	
PA	(REED/) REED J C.
XX	
PI	Reed JC;
XX	

DR WPI: 1995-139394/18.
XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT of human solid tumours, esp. breast cancer
XX
XX
PS Example 12; Page 33; 108pp; English.
CC Antisense oligonucleotides were tested for their ability to induce
CC programmed cell death (DNA fragmentation) in the human lymphoma cell
CC line RS1846. The oligonucleotides are phosphodiester targeted
CC against the translation initiation site (AAQ86650-55) or the 5'-cap
CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9gagaccctctctaccg 17
Db 1 9gagaccctctctaccg 17
|||||

RESULT 2
AAV28177
ID AAV28177 standard; DNA: 17 BP.
XX
XX AAV28177;
XX
XX 08-OCF-1998 (first entry)
XX
XX Antisense oligonucleotide to bcl-2 mRNA.
DE
XX
XX Purification: oligonucleotide: matrix; affinity unit;
XX affinity purification; antisense; bcl-2; ss.
XX
XX Synthetic.
XX
XX WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
XX
XX WPI: 1998-362922/31.
XX
XX Matrix for selective separation of oligo:nucleotide - useful for,
XX e.g. large scale purification of anti-sense agents from their
XX deletion derivatives formed during synthesis
XX
XX
XX Disclosure; Page 83; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
XX method of the invention. The specification describes a matrix that
XX comprises a support and an affinity unit that specifically and
XX reversibly binds a target oligonucleotide, and comprises a sequence of
XX bases having the reverse complement of a hybridising portion of the
XX target oligonucleotide. The matrix is used for affinity purification of
XX synthetic oligonucleotides, specifically antisense agents, for treatment
XX of hyperproliferative diseases, for treating a non-pathogen,
XX non-hyperproliferative disease, e.g. Alzheimer's, for modulating
XX expression of cell surface proteins, and to inhibit a eukaryotic
XX pathogen, retrovirus or other viruses.
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 9gagaccctctctaccg 17
Db 1 9gagaccctctctaccg 17
|||||

RESULT 3
AAV23689
ID AAV23689 standard; DNA: 17 BP.
XX
XX AAV23689;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 142.
DE
XX
XX Deletion sequence oligonucleotide: sensor array; eukaryotic pathogen;
XX probe; cellular adhesion modulator; cellular proliferation modulator;
XX human retrovirus; human immunodeficiency virus; non-human retrovirus;
XX HIV; primer; ss.
XX
XX Synthetic.
XX
XX WO9911820-A1.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 96WO-US18084.
XX
XX 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX
XX WPI: 1999-205198/17.
XX
XX New compositions comprising sensor arrays made up of unique probe
XX oligonucleotides - useful for characterizing a sample of target
XX deletion oligonucleotides
XX
XX Example 9; Page 151; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
XX sensor arrays, where each array comprises a unique probe
XX oligonucleotide, which is the reverse complement of part of a unique
XX target oligonucleotide present in a mixture of target deletion sequence
XX oligonucleotides. The compositions form a method for characterizing a
XX sample of target deletion oligonucleotides which are labelled and
XX hybridize with the probe oligonucleotides of the sensor arrays. Such
XX oligonucleotides and their targets are represented in AAV23548-X23709.
XX Oligonucleotides characterized by the method form pharmaceutical
XX compositions that are useful for modulating cellular adhesion or
XX proliferation, and being active against a eukaryotic pathogen, a human
XX retrovirus, a human immunodeficiency virus (HIV), or a non-human
XX retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
XX Syncytial Virus or cytomegalovirus (CMV). The compositions enable
XX characterization of deletion sequence oligonucleotides having related,
XX but different nucleobase sequences, and quantification of different
XX species of deletion sequence ("target") oligonucleotides in a mixture.
XX Also, if the specificity of the oligonucleotide's nucleobase sequence
XX for its reverse complement is not modified, the method may be performed
XX using oligodeoxynucleotides.
XX
XX Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;
SQ

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacccctctaccg 17
|||||
Db 1 ggagacccctctaccg 17

RESULT 4

AAx18698
ID AAX18698 standard; DNA; 17 BP.

AC AAX18698;

DT 10-MAY-1999 (first entry)

DE Target bcl-2 antisense oligonucleotide #30.

XX Cellular adhesion protein; proliferation; antisense oligonucleotide;

KW alimentary canal; transport; gastrointestinal mucosa; cancer;

KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;

KW HIV; inflammation; ss.

XX Synthetic.

XX WO9901579-A1.

XX 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13574.

XX 01-JUL-1997; 97US-0886829.

XX (ISIS-) ISIS PHARM INC.

XX Hardee G, Teng C;

XX WPI, 1999-106077/09.

PT Composition comprising nucleic acid and penetration enhancer - used particularly for delivering therapeutic antisense oligonucleotides across the gastrointestinal mucosa, provides high bioavailability

PS Example 2: Page 85; 115pp; English.

XX A pharmaceutical composition has been developed which comprises a nucleic acid and at least one penetration enhancer. The compositions are used: (i) to treat or prevent any disease or disorder that can be treated with the nucleic acid, e.g. cancer, Alzheimer's disease, beta-thalassemia, malaria, viral infections (including human immune deficiency virus (HIV)), inflammation, in human or animal medicine; (ii) to investigate the role of a gene or gene product in non-human animals; and (iii) to modulate gene expression in cells, tissues or organs. The compositions provide bioavailability of at least 15, preferably 17-35,%. The penetration enhancer improves: (i) transport of the nucleic acid across the mucosa of the alimentary canal and into cells; and (ii) increases stability of the nucleic acid. Oral administration avoids the complications and expense of intravenous or other methods of administration. AAX18698 to AAX18799 and AAX18801 represent antisense oligonucleotides which can be used as the nucleic acid in the method of the invention.

CC Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 other;

Query Match 100.0%; Score 17; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacccctctaccg 17
|||||
Db 1 ggagacccctctaccg 17

RESULT 5

AAQ86654
ID AAQ86654 standard; DNA; 17 BP.

AC AAQ86654;

DT 27-SEP-1995 (first entry)

DE Bcl-2 antisense oligonucleotide.

XX Anticod oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;

KW lymphoma; programmed cell death; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc-feature 1..17 /tag- a

FT /note- "3'-5' (antisense) sequence"

XX WO9508350-A.

XX 30-MAR-1995.

XX 20-SEP-1994; 94WO-US10725.

XX 20-SEP-1993; 93US-0124256.

XX (REED/) REED J C.

XX Reed JC;

XX WPI, 1995-139394/18.

XX Anti-code oligomers which bind to bcl-2 mRNA - for the treatment of human solid tumours, esp. breast cancer

PS Example 12: Page 33; 108pp; English.

XX Antisense oligonucleotides were tested for their ability to induce programmed cell death (DNA fragmentation) in the human lymphoma cell line RS1846. The oligonucleotides are phosphodiester targeted against the translation initiation site (AAQ86650-55) or the 5'-cap region (AAQ86656-58) of human bcl-2 pre-mRNAs.

CC region (AAQ86656-58) of human bcl-2 pre-mRNAs.

CC Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 16; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gacccctctaccg 17
|||||
Db 1 gacccctctaccg 14

RESULT 6

AAV28176
ID AAV28176 standard; DNA; 17 BP.

AC AAV28176;

DT 08-OCT-1998 (first entry)

DE Antisense oligonucleotide to bcl-2 mRNA.

XX Purification: oligonucleotide; matrix; affinity unit;

KW affinity purification; antisense; bcl-2; ss.

XX Synthetic.

PN WO9827425-A1.
XX
XX 25-JUN-1998.
XX
XX 18-DEC-1997; 97WO-US23284.
XX
XX 19-DEC-1996; 96US-0769951.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Cole DL, Srivatsa GS;
XX
XX WPI; 1998-362922/31.
XX
XX Matrix for selective separation of oligo:nucleotide - useful for,
PT e.g. large scale purification of anti-sense agents from their
PT deletion derivatives formed during synthesis
XX
XX Disclosure; Page 82; 183pp; English.
XX
XX AAV28155-268 represent oligonucleotides which can be purified using the
CC method of the invention. The specification describes a matrix that
CC comprises a support and an affinity unit that specifically and
CC reversibly binds a target oligonucleotide, and comprises a sequence of
CC bases having the reverse complement of a hybridising portion of the
CC target oligonucleotide. The matrix is used for affinity purification of
CC synthetic oligonucleotides, specifically antisense agents, for treatment
CC of hyperproliferative diseases, for treating a non-pathogen,
CC non-hyperproliferative disease, e.g. Alzheimer's, for modulating
CC expression of cell surface proteins, and to inhibit a eukaryotic
CC pathogen, retrovirus or other viruses.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 82.4%; Score 14; DB 19; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 gacccctctaccg 17
DB 1 gacccctctaccg 14

RESULT 7
AA18697
ID AAX23688 standard; DNA; 17 BP.
XX
XX AAX23688;
XX
XX 18-JUN-1999 (first entry)
XX
XX Deletion sequence oligonucleotide 141.
XX
XX Deletion sequence oligonucleotide; sensor array; eukaryotic pathogen;
KW probe; cellular adhesion modulator; cellular proliferation modulator;
KW human retrovirus; human immunodeficiency virus; non-human retrovirus;
KW HIV; primer; ss.
XX
XX Synthetic.
XX
XX WO9911820-A1.
XX
XX 11-MAR-1999.
XX
XX 01-SEP-1998; 98WO-US18084.
XX
XX 02-SEP-1997; 97US-0923771.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Chen D, Srivatsa GS;
XX

DR WPI; 1999-205198/17.
XX
XX New compositions comprising sensor arrays made up of unique probe
PT oligonucleotides - useful for characterizing a sample of target
PT deletion oligonucleotides
XX
XX Example 9; Page 150; 163pp; English.
XX
XX This invention describes a novel composition comprising a number of
CC sensor arrays, where each array comprises a unique probe
CC oligonucleotide, which is the reverse complement of part of a unique
CC target oligonucleotide present in a mixture of target deletion sequence
CC oligonucleotides. The compositions form a method for characterizing a
CC sample of target deletion oligonucleotides which are labelled and
CC hybridize with the probe oligonucleotides of the sensor arrays. Such
CC oligonucleotides and their targets are represented in AAX23548-X23709.
CC Oligonucleotides characterized by the method form pharmaceutical
CC compositions that are useful for modulating cellular adhesion or
CC proliferation, and being active against a eukaryotic pathogen, a human
CC retrovirus, a human immunodeficiency virus (HIV), or a non-human
CC retrovirus, including influenza virus, Epstein-Barr virus, Respiratory
CC Syncytial Virus or cytomegalovirus (CMV). The compositions enable
CC characterization of deletion sequence oligonucleotides having related,
CC but different nucleobase sequences, and quantification of different
CC species of deletion sequence ("target") oligonucleotides in a mixture.
CC Also, if the specificity of the oligonucleotide's nucleobase sequence
CC for its reverse complement is not modified, the method may be performed
CC using oligodeoxynucleotides.
XX
XX Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;
SQ

Query Match 82.4%; Score 14; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 gacccctctaccg 17
DB 1 gacccctctaccg 14

RESULT 8
AA18697
ID AAX18697 standard; DNA; 17 BP.
XX
XX AAX18697;
XX
XX 10-MAY-1999 (first entry)
XX
XX Target bcl-2 antisense oligonucleotide #29.
XX
XX Cellular adhesion protein; proliferation; antisense oligonucleotide;
KW alimentary canal; transport; gastrointestinal mucosa; cancer;
KW Alzheimer's disease; beta-thalassemia; malaria; viral infection;
KW HIV; inflammation; ss.
XX
XX Synthetic.
XX
XX WO9901579-A1.
XX
XX 14-JAN-1999.
XX
XX 01-JUL-1998; 98WO-US13574.
XX
XX 01-JUL-1997; 97US-0886829.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Hardee G, Teng C;
XX
XX WPI; 1999-106077/09.
XX
XX Composition comprising nucleic acid and penetration enhancer - used
PT

PT particularly for delivering therapeutic antisense oligonucleotides
PR across the gastrointestinal mucosa, provides high bioavailability
XX
PS Example 2; Page 85; 115pp; English.

CC A pharmaceutical composition has been developed which comprises a
CC nucleic acid and at least one penetration enhancer. The compositions are
CC used: (i) to treat or prevent any disease or disorder that can be
CC treated with the nucleic acid, e.g. cancer, Alzheimer's disease,
CC beta-thalassemia, malaria, viral infections (including human immune
CC deficiency virus (HIV)), inflammation, in human or animal medicine;
CC (ii) to investigate the role of a gene or gene product in non-human
CC animals; and (iii) to modulate gene expression in cells, tissues or
CC organs. The compositions provide bioavailability of at least 15,
CC preferably 17-35%. The penetration enhancer improves: (i) transport of
CC the nucleic acid across the mucosa of the alimentary canal and into
CC cells; and (ii) increases stability of the nucleic acid. Oral
CC administration avoids the complications and expense of intravenous or
CC other methods of administration. AAX18669 to AAX18799 and AAX18801
CC represent antisense oligonucleotides which can be used as the nucleic
CC acid in the method of the invention.

XX
SQ Sequence 17 BP; 2 A; 8 C; 3 G; 4 T; 0 other;

Query Match 82.4%; Score 14; DB 20; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 gacacctctaccg 17
|||||
DB 1 gacacctctaccg 14

RESULT 9

AAFO2633 standard; DNA; 17 BP.

AAFO2633;

16-FEB-2001 (first entry)

Hammerhead ribozyme substrate #928.

Ribozyme; erythropoietin; granulocyte colony stimulating factor;
interferon alpha, ss.

Homo sapiens.

WO200061729-A2.

19-OCT-2000.

11-APR-2000; 2000WO-US09721.

12-APR-1999; 99US-0129390.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Zwick M, Pavco P, McSwiggen J;

WPI; 2000-647423/62.

Enzymatic and antisense nucleic acid inhibition of repressor genes,
useful for producing e.g. granulocyte colony stimulating factor

protein, interferon alpha and erythropoietin -

Claim 37; Page 77; 164pp; English.

The present invention relates to enzymatic and antisense nucleic acid
molecules that act as inhibitors of the expression of repressor genes
encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA
transcription factor gene, IRF-2 and/or the CATT Displacement

CC Protein (CDP). Inhibition of the repressors removes prevents
CC inhibition (and consequently increases expression of) genes involved in
CC the production of erythropoietin, granulocyte colony stimulating factor
CC protein and interferon alpha.

XX
SQ Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 other;

Query Match 75.3%; Score 12.8; DB 21; Length 17;

Best Local Similarity 87.5%; Pred. No. 1.7e+03; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 gagacctctaccg 17
|||||
DB 1 gagacctctaccg 16

RESULT 10

AAT29732 standard; DNA; 45 BP.

AAT29732;

16-AUG-1996 (first entry)

Rat clone 13 Hct-1 probe.

Hippocampus-associated protein; Hct-1; cytochrome-P450;

steroid transformation; neuropsychiatric disorder; cognition;
neurodegenerative disease; endocrine disorder; diagnosis;

probe, ss.

Synthetic.

WO9612810-A1.

02-MAY-1996.

18-OCT-1995; 95WO-GB02465.

19-OCT-1994; 94GB-0021093.

(UYED-) UNIV EDINBURGH.

Lathe R, Rose KA, Stapleton G;

WPI; 1996-230611/23.

Novel hippocampus-associated proteins, Hct-1 - related to
cytochrome(s) P450 and useful for catalytic transformation of
substrates

Disclosure; Page 28; 70pp; English.

A synthetic DNA probe (AAT29732) is based on a rat Hct-1 cDNA
clone (see also AAT29723), beginning 112 nt 5' from the polyA tail.

It can be used with a rat Hct-1 probe (AAT29729) and Nathan's mouse
Hct-1 (AAT29730) for in situ hybridizations to detect Hct-1 in
brain tissue.

Sequence 45 BP; 12 A; 15 C; 5 G; 13 T; 0 other;

Query Match 75.3%; Score 12.8; DB 17; Length 45;

Best Local Similarity 87.5%; Pred. No. 1.7e+03; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 gagacctctacc 16
|||||
DB 22 gagacctctacc 37

RESULT 11

AAH80008
ID AAH80008 standard; DNA: 51 BP.
XX
AC AAH80008;
XX
DT 19-SEP-2001 (first entry)
XX
DE Human DNA containing single nucleotide polymorphism SEQ ID NO. 623.
XX
KM Human: single nucleotide polymorphism: SNP: angiotensin;
KM 4-hydroxybutyrate; dehydrogenase; protein therapy;
KM adenosine triphosphate-dependent RNA helicase;
KM major histocompatibility complex Class I histocompatibility antigen; MHC;
KM phosphoglycerate kinase; immunosuppressive; immunostimulatory;
KM antineumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
KM antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine; ds.
XX
OS Homo sapiens.
XX
PN WO200148245-A2.
XX
PD 05-JUL-2001.
XX
PF 27-DEC-2000; 2000WO-US35346.
XX
PR 27-DEC-1999; 99US-0472688.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI: 2001-418297/44.
XX
PT Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
PT diseases and infections -
XX
PS Claim 1; Page 240; 484bp; English.
XX
CC The invention relates to nucleic acids (AAH9386-AAH80036) encoding
CC polymorphic variants of proteins (AAH98010-AAH98238) related to
CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
CC proteins have potential immunosuppressive, immunostimulatory,
CC antineumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
CC antileukemic, neuroprotective and antimicrobial activity and may be
CC useful in gene/protein therapy, vaccines, modulation of the expression
CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase,
CC major histocompatibility complex (MHC) Class I histocompatibility antigen
CC and/or phosphoglycerate kinase. Disorders that may be prevented,
CC diagnosed and/or treated by the above methods include multifactorial
CC diseases with a genetic component, such as autoimmune diseases (e.g.
CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers
CC of the bladder, brain, breast, colon and kidney, leukemia), diseases of
CC the nervous system, an infection of pathogenic organisms. They may also
CC be used to alter phenotypic traits such as longevity, appearance,
CC strength, speed and endurance.
XX
SQ Sequence 51 BP; 13 A; 14 C; 17 G; 7 T; 0 other;

Query Match 75.3%; Score 12.8; DB 22; Length 51;
Best Local Similarity 87.5%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctacc 16
IIIIIIIIIIIIIIII
DB 25 ggagaccctgctacc 40

RESULT 12
AAS04946
ID AAS04946 standard; DNA: 18 BP.
XX
AC AAS04946;
XX
DT 07-SEP-2001 (first entry)
XX
DE Neurofibromatosis (NF1) cDNA sequencing primer #31.
XX
KM Neurofibromatosis type 1; NF1; peripheral blood lymphocyte; PBL; EBV; ss;
KM Epstein-Barr virus; B-lymphoblastoid cell; phytohemagglutinin; PHA;
KM frame shift mutation; mis-sense mutation; silent mutation; PCR primer;
KM sequencing primer.
XX
OS Homo sapiens.
XX
PN WO200129251-A2.
XX
PD 26-APR-2001.
XX
PF 18-OCT-2000; 2000WO-EP10255.
XX
PR 18-OCT-1999; 99EP-0870216.
PR 05-JUN-2000; 2000EP-0870122.
PR 16-JUN-2000; 2000US-0211629.
XX
PA (UYGE-) UNIV GENT.
XX
PI Messiaen L, Callens T;
XX
DR WPI: 2001-300341/31.
XX
PT Mutation analysis of NF1 gene by treating EBV transformed
PT lymphoblastoid cell lines formed with lymphocytes of patient with
PT protein synthesis inhibitor, and obtaining peptides by translating
PT amplified RNA from cell line -
XX
PS Claim 9; Page 57; 102pp; English.
XX
CC The sequences represent neurofibromatosis type 1 (NF1) cDNA fragments and
CC PCR primers and sequencing primers for use in mutation analysis of NF1. A
CC method for mutation analysis of the NF1 gene involves isolating
CC peripheral blood lymphocytes (PBL) of a patient, establishing
CC Epstein-Barr virus (EBV) transformed B-lymphoblastoid cell line with
CC isolated PBL, or short-term culturing of PBL by phytohemagglutinin (PHA)
CC stimulation, treating the cell line or short-term culture with protein
CC synthesis inhibitor and immediately extracting RNA from the cultures. The
CC RNA is then amplified and peptide fragments are obtained by in vitro
CC transcription/translation of amplified fragments. Mutation analysis of
CC NF1 is used for detection of frame shift, mis-sense and silent mutations
CC in various exons of the gene. This is useful in screening for NF1
CC mutations in young children who are often oligosymptomatic. Efficacy of a
CC drug or agent can be identified by a screening process in which
CC modulation is monitored in vitro using cell systems in which the
CC defective NF1 gene is expressed. The sequences can be used to design
CC drugs which modulate NF1 activity, by using knowledge of the structure of
CC the NF1 protein and of specific defects of the various NF1 mutant
CC proteins. The method allows for reliable analysis of mutations that are
CC difficult to detect due to unstable or wrong-spliced transcripts.
XX
SQ Sequence 18 BP; 3 A; 6 C; 3 G; 6 T; 0 other;

Query Match 72.9%; Score 12.4; DB 22; Length 18;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggagaccctctcta 14
IIIIIIIIIIIIIIII
DB 4 ggtgaccctctcta 17

RESULT 13

AAV73521

ID AAV73521 standard; DNA: 20 BP.

AC AAV73521;

XX 22-MAR-2000 (first entry)

XX H. pylori vacA primer VALXR.

XX PCR primer; probe; vacA; cagA; detection; vacuolating toxin; VDg;

XX virulence determinant gene; cytotoxin-associated gene; allele-specific;

XX infectivity; pathogenicity; gastritis; gastric; duodenal; ulcer;

XX adenocarcinoma; mucosa-associated lymphoid tissue lymphoma; therapy;

XX S region; S1a; S1b; S1c; S2; M region; M1; M2; Ss.

XX Helicobacter pylori.

XX MO9816658-A2.

XX 23-APR-1998.

XX 10-OCT-1997; 97WO-EP05614.

XX 16-OCT-1996; 96EP-0870131.

XX 09-SEP-1997; 97EP-0870133.

XX (INNO-) INNOGENETICS NV.

XX (DDL-) DDL BV.

XX Quint W, Van Doorn L;

XX WPI: 1998-251300/22.

XX Method for detecting and/or typing Helicobacter pylori strains

XX comprises use of primers and probes based on vacA and cagA gene

XX Claim 2; Page 44; 122pp; English.

XX This invention describes a novel method for the detection and/or typing

XX of Helicobacter pylori strains present in a sample using PCR primers and

XX probes to detect regions of the vacuolating toxin (vacA) gene and other

XX virulence determinant genes (VDg) e.g. the cytotoxin-associated (cagA)

XX gene. The method allows the typing and allele-specific detection of a

XX strain according to the VDg alleles present in that particular H. pylori

XX strain. The virulence determinant genes are the genetic elements

XX involved in enabling, determining, and marking the infectivity and/or

XX pathogenicity of the H. pylori strain. The method provides a way of

XX detecting H. pylori strains in a sample with respect to the development

XX of chronic active gastritis, gastric and duodenal ulcers, gastric

XX adenocarcinomas, mucosa-associated lymphoid tissue lymphomas, and/or

XX determining eradication therapy. AAV73508-V73546 represent PCR primers

XX and probes used in the detection of the H. pylori vacA and cagA genes.

XX The primers and probes are used especially to detect the vacA S regions

XX S1a/b/c and S2 and the M regions M1 and M2 which are represented in

XX AAV73547-V73785.

XX Sequence 20 BP; 4 A; 8 C; 3 G; 4 T; 1 other;

XX Query Match

XX Best Local Similarity 81.2%; Score 12.4; DB 19; Length 20;

XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX QY 2 gagacccctctacg 17

XX 11:111 1111111 1

XX Db 4 garaccgtctctacag 19

ID AAZ26082 standard; DNA: 21 BP.

XX AAZ26082;

XX 30-NOV-1999 (first entry)

XX Human polymorphic region 271.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;

XX cell viability; loss of heterozygosity; precancerous condition; ASI;

XX allele specific inhibitor; somatic cell; diagnosis; prevention;

XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;

XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;

XX graft versus host disease; malignant cell removal; bone marrow; ss.

XX Homo sapiens.

XX WO9841648-A2.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-US05419.

XX 20-MAR-1997; 97US-0041057.

XX (VARI-) VARIAGENICS INC.

XX Housman D, Ledley FD, Stanton VP;

XX WPI: 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for

XX diagnosis, prevention and treatment of, e.g. cancers, atherosclerotic

XX plaque, dysplastic lesions, endometriosis or graft versus host disease

XX Disclosure; Figure 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor

XX potentially useful for treatment of cancer, where the inhibitor is

XX active on a gene vital for cell growth or viability, and where the gene

XX is subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is

XX used for preventing the development of cancer in a patient having a

XX precancerous condition, by administering to the patient a first allele

XX specific inhibitor (ASI) targeted to an allele of a first essential gene

XX present in cells of the precancerous condition, where the normal somatic

XX cells of the patient are heterozygous for the first gene, the inhibitor

XX is active on at least one but less than all allelic forms of the gene

XX present in a population and targets only one allelic form present in the

XX normal somatic cells, and the first gene. The products and methods can

XX be used in the diagnosis, prevention and treatment of LOH disorders,

XX e.g. cancers, atherosclerotic plaques, premalignant metaplastic or

XX dysplastic lesions, benign tumours, endometriosis, polycystic kidney

XX disease, and graft versus host disease. The method can also be used to

XX remove malignant cells from bone marrow transplants. AAZ25812-226825

XX represent human polymorphic sites described in the method of the

XX invention.

XX Sequence 21 BP; 6 A; 4 C; 8 G; 3 T; 0 other;

XX Query Match

XX Best Local Similarity 92.9%; Score 12.4; DB 19; Length 21;

XX Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX QY 2 gagacccctctacg 15

XX 111 11111111111 1

XX Db 15 GAGGCCCTTCTAC 2

RESULT 15

AA011413/c

ID AA011413 standard; DNA: 17 BP.

XX AA011413

AC AAD11413;
 XX
 DT 24-SEP-2001 (first entry)
 XX
 DE Plasmid B1154 disruption cassette amplifying PCR primer OSCXKS14.
 XX
 KW Five-carbon sugar; aldo-sugar; keto-sugar; sugar alcohol; fermentation;
 KW pentose phosphate pathway; xylitol; D-arabitol; D-arabinose; D-lyxose;
 KW ribitol; D-ribose; D-ribulose; D-xylose; D-xylulose; microbial host;
 KW arabitol phosphate dehydrogenase; APDH; xylitol phosphate dehydrogenase;
 KW APDH; PCR primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200153306-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 22-JAN-2001; 2001WO-FI00051.
 XX
 PR 21-JAN-2000; 2000US-0488581.
 XX
 PA (XYRO-) XYROFIN OY.
 XX
 PI Miasnikov A, Ojama H, Povelainen M, Gros H, Toivari M, Richard P;
 PI Ruohonen L, Kolivrantha K, Lonsborough J, Aristidou A;
 PI Penttilae M, Plazancet-Menut C, Deutscher J;
 XX
 DR WPI; 2001-465360/50.
 XX
 PT Isolated polynucleotide, used to transform bacterial or yeast hosts
 PT which can then be used in the production of sugars and sugar alcohols,
 PT encodes xylitol phosphate dehydrogenase -
 XX
 PS Example 12; Page 188; 205pp; English.
 XX
 CC The present invention relates to the methods for manufacturing
 CC five-carbon aldo- and keto-sugars and sugar alcohols by fermentation in
 CC recombinant hosts. The recombinant hosts of the invention have been
 CC engineered to enhance the production of the pentose phosphate pathway
 CC intermediates, or the production of one or more of xylitol, D-arabitol,
 CC D-arabinose, D-lyxose, ribitol, D-ribose, D-ribulose, D-xylose and/or
 CC D-xylulose. Arabitol phosphate dehydrogenase (APDH) is used in a
 CC microbial host cell to produce recombinant arabitol. Xylitol phosphate
 CC dehydrogenase (XPDH) and arabitol phosphate dehydrogenase are used in a
 CC microbial host cell to produce recombinant xylitol. The present sequence
 CC is a PCR primer which is used for the amplification of disruption
 CC cassette of plasmid B1154, used in the exemplification of the invention.
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 4 G; 3 T; 0 other;

Query Match 71.88; Score 12.2; DB 22; Length 17;
 Best Local Similarity 82.4%; Pred. No. 3.5e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ggagaccctcctaccg 17
 ||||| ||||| ||
 Db 17 GGAGATCCTTCTTAGCG 1

Search completed: June 28, 2002, 22:40:16
 Job time: 8092 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:16:49 ; Search time 334.55 Seconds
(without alignments)
12.482 Million cell updates/sec

Title: US-09-709-170A-13

Perfect score: 17

Sequence: 1 ggaagaccctctctacg 17

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 590990

Minimum DB seq length: 0

Maximum DB seq length: 75

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PTC05.COMB.seq:*

6: /cgn2_6/ptodata/1/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	2	US-08-465-485A-13
2	17	100.0	17	3	US-09-080-285-13
3	14	82.4	17	2	US-08-465-485A-12
4	14	82.4	17	3	US-09-080-285-12
5	12.8	75.3	45	2	US-08-845-161A-17
6	12.8	75.3	45	4	US-09-270-751-17
7	12.4	72.9	40	1	US-08-231-342-17
8	12.2	71.8	71	2	US-08-894-578-201
9	12	70.6	60	4	US-09-339-913B-26
10	12	70.6	60	4	US-09-339-904A-26
11	12	70.6	60	4	US-08-769-062B-26
12	12	70.6	60	4	US-09-344-002B-26
13	11.8	69.4	18	3	US-08-894-173-12
14	11.8	69.4	18	4	US-09-398-193-12
15	11.8	69.4	19	1	US-08-388-381-23
16	11.8	69.4	19	3	US-08-765-626-23
17	11.8	69.4	19	5	PCT-US95-08605-23
18	11.8	69.4	60	2	US-08-663-566A-40
19	11.8	69.4	60	2	US-08-023-610-40
20	11.8	69.4	60	2	US-08-288-065A-40
21	11.8	69.4	60	2	US-08-362-240A-40
22	11.8	69.4	60	5	PCT-US95-10245-40
23	11.8	69.4	74	4	US-09-315-793-14
24	11.4	67.1	20	3	US-09-418-641-82
25	11.4	67.1	26	2	US-08-859-998-100
26	11.4	67.1	26	4	US-09-225-928-100
27	11.4	67.1	32	2	US-08-305-764C-21

28	11.4	67.1	55	4	US-09-591-025-5	Sequence 5, Appl
29	11.4	67.1	70	4	US-09-025-769B-129	Sequence 129, App
30	11.2	65.9	19	3	US-09-290-449-11	Sequence 11, Appl
31	11.2	65.9	24	1	US-08-116-389-23	Sequence 23, Appl
32	11.2	65.9	24	1	US-08-708-431-23	Sequence 23, Appl
33	11.2	65.9	24	2	US-08-880-830-23	Sequence 23, Appl
34	11.2	65.9	24	5	PCT-US94-13895-23	Sequence 23, Appl
35	11.2	65.9	25	1	US-08-276-919-11	Sequence 11, Appl
36	11.2	65.9	25	1	US-08-776-088-16	Sequence 16, Appl
37	11.2	65.9	25	5	PCT-US95-09145A-16	Sequence 16, Appl
38	11.2	65.9	27	1	US-08-116-389-22	Sequence 22, Appl
39	11.2	65.9	27	1	US-08-169-303-6	Sequence 6, Appl
40	11.2	65.9	27	1	US-08-708-431-22	Sequence 22, Appl
41	11.2	65.9	27	2	US-08-880-830-22	Sequence 22, Appl
42	11.2	65.9	27	2	US-08-791-883-3	Sequence 3, Appl
43	11.2	65.9	27	3	US-09-023-673-3	Sequence 3, Appl
44	11.2	65.9	27	5	PCT-US94-13895-22	Sequence 22, Appl
45	11.2	65.9	48	1	US-07-618-946B-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-08-465-485A-13

Sequence 13, Application US/08465485A

Patent No. 5831066

GENERAL INFORMATION:

APPLICANT: Reed, John

TITLE OF INVENTION: Regulation of bcl-2 Gene Expression

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. Jefferson Davis Hwy., Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,485A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/124,256

FILING DATE: 20-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/840,716

FILING DATE: 21-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/288,692

FILING DATE: 22-DEC-1988

ATTORNEY/AGENT INFORMATION:

NAME: Fortney, Andrew D.

REGISTRATION NUMBER: 34,600

REFERENCE/DOCKET NUMBER: 3335-070-55 CONT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (408) 436-2070

TELEFAX: (408) 436-2075

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ANTI-SENSE: YES

US-08-465-485A-13

Query Match 100.0%; Score 17; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacctctaccg 17
|||||
Db 1 GGAGACCTTCTACCG 17

RESULT 2

US-09-080-285-13
; Sequence 13, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/080,285
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,485
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-09-080-285-13

Query Match 100.0%; Score 17; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ggagacctctaccg 17
|||||
Db 1 GGAGACCTTCTACCG 17

RESULT 3

US-08-465-485A-12
; Sequence 12, Application US/08465485A
; Patent No. 5831066
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Hwy., Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,485A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/124,256
; FILING DATE: 20-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/840,716
; FILING DATE: 21-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/288,692
; FILING DATE: 22-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ANTI-SENSE: YES
; US-08-465-485A-12

Query Match 82.4%; Score 14; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gacctctctaccg 17
|||||
Db 1 GACCTTCTACCG 14

RESULT 4

US-09-080-285-12
; Sequence 12, Application US/09080285
; Patent No. 6040181
; GENERAL INFORMATION:
; APPLICANT: Reed, John
; TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-12

Query Match 82.4%; Score 14; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gaccctctacg 17
|||||
Db 1 GACCCTCTACCG 14

RESULT 5
US-08-845-161A-17
Sequence 17, Application US/08845161A
Patent No. 5976850
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Rose, Kenneth A.
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS: DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 5976850th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-845-161A-17

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,161A
FILING DATE: 21-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-845-161A-17

Query Match 75.3%; Score 12.8; DB 2; Length 45;
Best Local Similarity 87.5%; Pred. No. 1,6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggaagaccctctac 16
|||||
Db 22 GGAGTCCATCCTACC 37

RESULT 6
US-09-270-751-17
Sequence 17, Application US/09270751
Patent No. 6184350
GENERAL INFORMATION:
APPLICANT: Lathe, Richard
APPLICANT: Rose, Kenneth A.
TITLE OF INVENTION: HIPPOCAMPUS-ASSOCIATED PROTEINS: DNA
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USED THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 No. 6184350th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,751
FILING DATE: 17-APR-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02465
FILING DATE: 18-OCT-1995
APPLICATION NUMBER: GB 9421093.7
FILING DATE: 19-OCT-1994
ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 604-408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4100
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-270-751-17

Query Match 75.3%; Score 12.8; DB 4; Length 45;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagacctctacc 16
|||||
Db 22 GGAGTCCCATCTACC 37

RESULT 7
US-08-231-342-17/C
Sequence 17, Application US/08231342
Patent No. 5827684
GENERAL INFORMATION:
APPLICANT: Sreekrishna, Kotikanyadanam
APPLICANT: Prevatt, William D
APPLICANT: Thill, Gregory P
APPLICANT: Davis, Geneva R
APPLICANT: Koutz, Patricia
APPLICANT: Barr, Kathryn A
APPLICANT: Hopkins, Sharon A
TITLE OF INVENTION: Production of Bacillus Entomotoxins in
TITLE OF INVENTION: Methylotrophic Yeast
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 135 S. LaSalle St.
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603-4277
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,342
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/926,448
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Feder, Scott B
REGISTRATION NUMBER: 33,129
REFERENCE/DOCKET NUMBER: 52627
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEFAX: 312-372-7848
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
US-08-231-342-17

Query Match 72.9%; Score 12.4; DB 1; Length 40;
Best Local Similarity 92.9%; Pred. No. 2.7e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gacctctaccg 17
|||||
Db 40 GACCTTCTTACCG 27

RESULT 8
US-08-894-578-201
Sequence 201, Application US/08894578
Patent No. 5998142
GENERAL INFORMATION:
APPLICANT: GOLD et al.
TITLE OF INVENTION: SYSTEMATIC EVOLUTION OF LIGANDS
TITLE OF INVENTION: BY EXPONENTIAL ENRICHMENT:
NUMBER OF SEQUENCES: 226
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG
COMPUTER: IBM pc compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,578
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: PCT/US96/03097
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,935
FILING DATE: 17-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: 22-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/234,997
FILING DATE: 28-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/309,245
FILING DATE: 20-SEPTEMBER-1994
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX28/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs

;; PRIOR FILING DATE: 1996-12-18
;; PRIOR APPLICATION NUMBER: 08/198,431
;; PRIOR FILING DATE: 1994-02-17
;; PRIOR APPLICATION NUMBER: 08/425,684
;; PRIOR FILING DATE: 1995-04-18
;; PRIOR APPLICATION NUMBER: 08/537,874
;; PRIOR FILING DATE: 1995-10-30
;; NUMBER OF SEQ ID NOS: 101
;; SOFTWARE: Patentln Ver. 2.0
;; SEQ ID NO: 26
;; LENGTH: 60
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: degenerate
;; OTHER INFORMATION: oligonucleotide used for codon usage library
US-09-344-002B-26

Query Match
Best Local Similarity 70.6%; Score 12; DB 4; Length 60;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 ggagaccctctctac 16
| :||:||||:|:|:
Db 20 gargayccctcytc 35

RESULT 13
US-08-894-173-12
;; Sequence 12, Application US/08894173A
;; Patent No. 6090612
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; TITLE OF INVENTION: Adenylate cyclase and uses therefor
;; FILE REFERENCE: P14716C
;; CURRENT APPLICATION NUMBER: US/08/894,173A
;; CURRENT FILING DATE: 1997-08-13
;; NUMBER OF SEQ ID NOS: 97
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO: 12
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: STRANDEDNESS : Single
;; FEATURE:
;; OTHER INFORMATION: TOPOLOGY : Linear
;; FEATURE:
;; OTHER INFORMATION: MOLECULE TYPE : CDNA
;; FEATURE:
;; OTHER INFORMATION: HYPOTHETICAL : NO
;; FEATURE:
;; OTHER INFORMATION: ANTI-SENSE : YES
;; FEATURE:
;; OTHER INFORMATION: CELL LINE : A120
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer to
;; OTHER INFORMATION: 1kb extension of cDNA clone jpl34 of A120
US-08-894-173-12

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 3; Length 18;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctctac 15
||||| |||||
Db 1 ggagagactctctac 15

RESULT 14
US-09-398-193-12

;; Sequence 12, Application US/09398193
;; Patent No. 6197581
;; GENERAL INFORMATION:
;; APPLICANT: Medical Research Council
;; TITLE OF INVENTION: Adenylate cyclase and uses therefor
;; FILE REFERENCE: P24360-
;; CURRENT APPLICATION NUMBER: US/09/398,193
;; CURRENT FILING DATE: 1999-09-17
;; NUMBER OF SEQ ID NOS: 104
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO: 12
;; LENGTH: 18
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: STRANDEDNESS : Single
;; FEATURE:
;; OTHER INFORMATION: TOPOLOGY : Linear
;; FEATURE:
;; OTHER INFORMATION: MOLECULE TYPE : CDNA
;; FEATURE:
;; OTHER INFORMATION: HYPOTHETICAL : NO
;; FEATURE:
;; OTHER INFORMATION: ANTI-SENSE : YES
;; FEATURE:
;; OTHER INFORMATION: CELL LINE : A120
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer to
;; OTHER INFORMATION: 1kb extension of cDNA clone jpl34 of A120
US-09-398-193-12

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 4; Length 18;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ggagaccctctctac 15
||||| |||||
Db 1 ggagagactctctac 15

RESULT 15
US-08-388-381-23/c
;; Sequence 23, Application US/08388381
;; Patent No. 5552283
;; GENERAL INFORMATION:
;; APPLICANT: Diamond's, Eleftherios
;; APPLICANT: Dunn, James M.
;; APPLICANT: Stevens, John K.
;; TITLE OF INVENTION: Method, Reagents and Kit for Diagnosis
;; TITLE OF INVENTION: and Targeted Screening for p53 Mutations
;; NUMBER OF SEQUENCES: 41
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Oppedahl & Larson
;; STREET: 1992 Commerce Street, Suite 309
;; CITY: Yorktown Heights
;; STATE: NY
;; COUNTRY: USA
;; ZIP: 10598-4412
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS 5.0
;; SOFTWARE: Word Perfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/388,381
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/271,946
;; FILING DATE: 08-JUL-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Marina T. Larson

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;
; REGISTRATION NUMBER: 32,038
; REFERENCE/DOCKET NUMBER: VGEN.P-003-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (914) 245-3252
; TELEFAX: (914) 962-4330
;
; TELEX:
;
; INFORMATION FOR SEQ ID NO: 23:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 19
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; HYPOTHEICAL: no
; ANTI-SENSE: yes
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; NAME/KEY: sequencing primer for exon 2 of human p53 gene
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US-08-388-381-23

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Query Match 69.4%; Score 11.8; DB 1; Length 19;
Best Local Similarity 86.7%; Pred. No. 5.2e+02;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 2 gagaccttctacc 16
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Db 19 GAGACGCTTCCAACC 5

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Search completed: June 28, 2002, 22:16:50
Job time: 8276 sec

11

Query Match	100.0%;	Score 15;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 2.9e+04;		

	Matches	15; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	gcgcgcgcacgcgcg	15						
Db	1	gcgcgcgcgcgcgcgcg	15						

RESULT	2		
AX107320			
LOCUS	AX107320	33 bp	DNA
DEFINITION	Sequence 139 from Patent WO0123606.		linear
ACCESSION	AX107320		
VERSION	AX107320.1	GI:13922805	
KEYWORDS			
SOURCE			
ORGANISM	Pectobacterium chrysanthemi.		
	Pectobacterium chrysanthemi		

REFERENCE	1 (bases 1 to 33)
AUTHORS	Grabowski, R. and Berghof, K.
TITLE	Nucleic acid molecules for detecting bacteria and phylogenetic
JOURNAL	units of bacteria
FEATURES	Patent: WO 0123606-A 139 05-APR-2001;
source	Biotecon Diagnostics GmbH (DE)
	location/Qualifiers
	1..33
	/organism="Pectobacterium chrysanthemi"
	/db_xref="taxon:556"
BASE COUNT	3 a 11 c 14 g 5 t
ORIGIN	

	Query Match	Score	DB	Length
	89.3%	13.4	6	33
	Best Local Similarity	93.3%	Pred. No. 1	1e+05
	Matches	14	Conservative	0
			Mismatches	1
			Indels	0
			Gaps	0
Ox	1 gcgcgcgcacgcgcg	15		
db	6 gcgcgcgcgcgcgcg	20		

RESULT	3				
AX099682/c					
LOCUS	AX099682	40 bp	DNA	linear	PAT 02-APR-2001
DEFINITION	Sequence	38 from Patent WO0119976.			
ACCESSION	AX099682				
VERSION	AX099682.1	GI:13538736			
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
REFERENCE	artificial sequence.				
AUTHORS	1 (bases 1 to 40)				
TITLE	Anderson,H.M., Chay,C.A., Chen,G. and Conner,T.W.				
JOURNAL	Plant regulatory sequences for control of gene expression				
	Patent: WO 0119976-A 38 22-MAR-2001;				
	MONSANTO COMPANY (US).				

source	1. .40			
	/organism="synthetic construct"			
	/db_xref="taxon:32630"			
	/note="primer"			
BASE COUNT	3 a	17 c	13 g	7 t
ORIGIN				

	Query Match	Score	DB	Length
	Best Local Similarity	93.3%	1e+05	
Matches	14; conservative	0;	Mismatches 1;	Indels 0;
QY	1 gcgcgcgcgcgcgcgcg	15		
db	26 gcgcgcgcgcgcgcgcg	12		

	RESULT	4					
AR052628	LOCUS	AR052628	20 bp	DNA	linear	PAT 29-SEP-1999	
	DEFINITION	Sequence from patent US 5831066.					
	ACCESSION	AR052628					
	VERSION	AR052628.1	GI:5975992				
	KEYWORDS						

REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source
1	(bases 1 to 20)	unclassified.			
	Reed, J.C.	Regulation of bcl-2 gene expression			
	Patent: US 5831066-A	28 03-NOV-1998;			
	Location/Qualifiers				
	1..20				
	/organism="unknown"				
BASE COUNT	2 a	7 c	11 g	0 t	
ORIGIN					

Query Match	86.7%;	Score 13;	DB 6;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.9e+05;		
Matches	13;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	gagagcagcagc	13	
Db	8	gcgcgcgcaccc	20	

[illegible]

Query Match	82.7%	Score 12.4	DB 6	Length 20
Best Local Similarity	92.9%	Pred. No. 3.5e+05		
Matches 13, Conservative	0	Mismatches 1	Indels 0	Gaps 0
QY 1 gcgcgcgcacgcgcg 14				
Db 7 GCgcgcgcgcgcgcg 20				

LOCUS	AX146640	RESULT 6
DEFINITION	AX146640	25 bp DNA
ACCESSION	Sequence 16 from Patent WO0134817.	linear
VERSION	AX146640	PAT 31-MAY-2001
KEYWORDS	AX146640.1 GI:14285033	
SOURCE	.	
ORGANISM	Zea mays. Zea mays.	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Clade; Panicoideae; Andropogoneae; Zea.	

REFERENCE 1 (bases 1 to 25)
AUTHORS helent Jaris,T.G.
TITLE Genes encoding enzymes for lignin biosynthesis and uses thereof
JOURNAL Patent: WO 0134817-A 16 17-MAY-2001;
PIONEER HI-BRED INTERNATIONAL, INC. (US)
FEATURES
source 1..25
/organism="zea mays"
/db_xref="taxon:4577"
BASE COUNT 4 a 7 c 10 g 4 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 25;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cgcgcgacgacgcg 14
|||||
Db 10 GCGCGGCGACGCG 23

RESULT 7
AX147141 30 bp DNA linear PAT 08-JUN-2001
LOCUS AX147141
DEFINITION Sequence 99 from Patent WO0136481.
ACCESSION AX147141
VERSION AX147141.1 GI:14346317
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong,Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 99 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 7 c 15 g 1 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgcgacgacgcg 15
|||||
Db 7 CAGCGGCGACGCGG 20

RESULT 8
AX147142 30 bp DNA linear PAT 08-JUN-2001
LOCUS AX147142
DEFINITION Sequence 100 from Patent WO0136481.
ACCESSION AX147142
VERSION AX147142.1 GI:14346318
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong,Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 100 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 7 c 15 g 1 t
ORIGIN

source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 1 a 15 c 7 g 7 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgcgacgacgcg 15
|||||
Db 24 CAGCGGCGACGCGG 11

RESULT 9
AX147155 30 bp DNA linear PAT 08-JUN-2001
LOCUS AX147155
DEFINITION Sequence 113 from Patent WO0136481.
ACCESSION AX147155
VERSION AX147155.1 GI:14346326
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong,Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 113 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 1 a 15 c 7 g 7 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgcgcgacgacgcg 15
|||||
Db 24 CAGCGGCGACGCGG 11

RESULT 10
AX147156 30 bp DNA linear PAT 08-JUN-2001
LOCUS AX147156
DEFINITION Sequence 114 from Patent WO0136481.
ACCESSION AX147156
VERSION AX147156.1 GI:14346327
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong,Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 114 25-MAY-2001;
Wong, Yung Hou (CN)
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"
BASE COUNT 7 a 7 c 15 g 1 t
ORIGIN

ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgagcgagcgagcg 15
1 | | | | | | | | | |
Db 7 CAGCGGCGAGCGCGG 20

RESULT 11
AX147157/c 30 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 115 from Patent WO0136481.
DEFINITION AX147157
ACCESSION AX147157
VERSION AX147157.1 GI:14346328
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 115 25-MAY-2001;
Mong, Yung Hou (CN)
FEATURES
location/Qualifiers
1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"

BASE COUNT 1 a 15 c 7 g 7 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgagcgagcgagcg 15
1 | | | | | | | | | |
Db 24 CAGCGGCGAGCGCGG 11

RESULT 12
AX147158 30 bp DNA linear PAT 08-JUN-2001
LOCUS Sequence 116 from Patent WO0136481.
DEFINITION AX147158
ACCESSION AX147158
VERSION AX147158.1 GI:14346329
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wong, Y.H.
TITLE Novel chimeric g-alpha proteins displaying increased promiscuity
JOURNAL Patent: WO 0136481-A 116 25-MAY-2001;
Mong, Yung Hou (CN)
FEATURES
location/Qualifiers
1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="PCR primer"

BASE COUNT 7 a 15 g 1 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 30;
Best Local Similarity 92.9%; Pred. No. 3.2e+05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 cgagcgagcgagcg 15
1 | | | | | | | | | |
Db 7 CAGCGGCGAGCGCGG 20

RESULT 13
A91129/c 70 bp DNA linear PAT 22-JAN-2000
LOCUS Sequence 8 from Patent WO9827225.
DEFINITION A91129
ACCESSION A91129
VERSION A91129.1 GI:6740159
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 70)
AUTHORS Cardy, D.L.
TITLE ASSAY INVOLVING LOOPED NUCLEIC ACID
JOURNAL Patent: WO 9827225-A 8 25-JUN-1998;
CARDY DONALD LEONARD NICHOLAS (GB); CYTOCELL LTD (GB)
FEATURES
location/Qualifiers
1..70
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 2 a 26 c 26 g 16 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cgagcgagcgagcg 15
1 | | | | | | | | | |
Db 70 CGAGCGGCGAGCGCGG 57

RESULT 14
AR081378 70 bp DNA linear PAT 31-AUG-2000
LOCUS Sequence 37 from patent US 5972599.
DEFINITION AR081378
ACCESSION AR081378
VERSION AR081378.1 GI:10008104
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 70)
AUTHORS Tasset, D., Pagratidis, N., Jayasena, S. and Gold, L.
TITLE High affinity nucleic acid ligands of cytokines
JOURNAL Patent: US 5972599-A 37 26-OCT-1999;
FEATURES
location/Qualifiers
1..70
/organism="unknown"

BASE COUNT 13 a 16 c 31 g 10 t
ORIGIN

Query Match 82.7%; Score 12.4; DB 6; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gggcgagcgagcg 14
1 | | | | | | | | | |
Db 12 GCGGTCGAGCGCGG 25

RESULT 15
MZETACAT 74 bp DNA linear PLN 27-APR-1993
LOCUS MZETACAT
DEFINITION Z.mays transposon Ac insertion sequence 1, allele bz-m2(Ac).

AAH49944
ID AAH49944 standard; DNA: 33 BP.
XX
AC AAH49944;
XX
DT 22-AUG-2001 (first entry)
XX
DE Bacterial 23S/5S RNA detecting primer SEQ ID 139.
XX
KM Detection: spacer: 23S rDNA; 5S rDNA; probe: phylogenetic group;
XX enterobacterium; clinical diagnosis; food contamination; ss.
XX Erwinia chrysanthemi.
OS
PN DE19945916-A1.
XX
PD 05-APR-2001.
XX
PF 24-SEP-1999; 99DE-1045916.
XX
PR 24-SEP-1999; 99DE-1045916.
XX
PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI Grabowski R, Berghof K;
XX
DR WPI; 2001-246133/26.
XX
PT New nucleic acid primers and probes, useful for bacterial detection, in
PT clinical diagnosis and detecting food contamination, comprises 23S and
PT 5S rDNA sequences -
XX
XX
PS Claim 17; Page 63; 140pp; German.
XX
CC This invention describes a novel nucleic acid molecule (I), useful as a
CC probe and/or primer for detecting bacteria. The invention also describes
CC (1) a combination of at least two nucleic acids (II) for detecting
CC bacteria or phylogenetic groups of bacteria, particularly enterobacteria;
CC (2) a kit containing (I) or the combination of (II); (3) detecting
CC bacteria (particularly enterobacteria) in a sample by contacting the
CC sample with (I) or the combination of (II) and detecting hybridization;
CC and (4) amplifying (MI) bacterial DNA from many different taxonomic
CC groups using (I) or the combination of (II) as primers. The method is
CC used to detect and identify bacteria, for clinical diagnosis and for
CC detecting contamination of food. (I) can detect bacteria at various
CC levels of selectivity (e.g., all bacteria, particular classes, families,
CC genera or species). The method exploits the fact that the 23S and 5S rDNA
CC regions, and the intermediate transcribed spacer, contain some sequences
CC that are highly conserved and others that are highly variable.
CC AAH49807-AAH50411 represent primers used to illustrate the method of the
CC invention.
XX
XX
SQ Sequence 33 BP; 3 A; 11 C; 14 G; 5 T; 0 other.

Query Match 89.3%; Score 13.4; DB 22; Length 33;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 15
| | | | | | | | | | |
Db 6 ggcggcgagcgagcg 20

RESULT 7
ID AAF81441/C
XX AAF81441 standard; DNA: 40 BP.
XX
AC AAF81441;
XX
XX
DT 08-JUN-2001 (first entry)
XX
DE PCR primer GSP2 for corn promoter clone #700164205.

XX
XX Corn; promoter; transgenic plant; herbicide resistance; PCR primer; ss.
XX
XX Zea mays.
OS
XX
XX WO200119976-A2.
PN
XX
PD 22-MAR-2001.
XX
XX
PF 13-SEP-2000; 2000WO-US25078.
XX
PR 16-SEP-1999; 99US-0154182.
XX
XX
PA (MONS) MONSANTO CO.
XX
PI Anderson HM, Chay CA, Chen G, Conner TW;
XX
XX WPI; 2001-244796/25.
DR
XX
XX Novel promoter nucleic acid sequences useful for regulating
PT heterologous gene expression in plants, comprising regulatory sequences
PT located upstream to plant DNA structural coding sequences -
XX
XX
PS Example 3; Page 87; 101pp; English.
XX
XX The present invention relates to novel corn promoter sequences (see
CC AAF81456-AAF81478). The promoter sequences are useful for conferring
CC expression of a second polynucleotide molecule in a transgenic plant
CC tissue. In addition, the promoter sequences are useful for providing
CC plants with herbicide resistance. The promoter sequences are suitable for
CC selectively modulating expression of any operatively linked gene and
CC provide additional regulatory element diversity in a plant expression
CC vector in gene stacking approaches. The present sequence is a PCR primer
CC used in the present invention.
XX
XX
SQ Sequence 40 BP; 3 A; 17 C; 13 G; 7 T; 0 other.

Query Match 89.3%; Score 13.4; DB 22; Length 40;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 15
| | | | | | | | | | |
Db 26 ggcggcgagcgagcg 12

RESULT 8
ID AAL29213
XX AAL29213 standard; DNA: 51 BP.
XX
AC AAL29213;
XX
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #2421.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
XX
OS Homo sapiens.
XX
XX WO200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US35498.

PR 03-APR-2001; 2001US-0825876.

PR	07-MAY-1998;	98US-0084641.
PR	03-MAY-1999;	99US-0304232.

PR	07-MAY-1998;	98US-0084641.
PR	03-MAY-1999;	99US-0304232.

PA (AFY-) AFFYMETRIX INC.
 PA (UYCA-) UNIV CASE WESTERN RESERVE.
 XX
 XX
 PI Fan JB, Chakravarti A, Haluska MK;
 XX
 DR WPI: 2000-107928/10.
 XX
 PT Novel nucleic acids containing polymorphisms used in the diagnosis of
 PT hypertension -
 XX
 PS Claim 1: Page 16; 53pp; English.
 CC The invention provides polymorphic fragments of genes associated with
 CC hypertension. The nucleic acids including the polymorphic sites can be
 CC used as probes or primers for expressing variant proteins. Detection of
 CC the polymorphisms is useful in designing prophylactic and therapeutic
 CC regimens customized to underlying abnormalities. The polymorphisms can be
 CC used for association studies for hypertension, and in hypertension
 CC diagnostic assays. Where the polymorphisms have strong correlation with
 CC hypertension, within a gene, they are likely to have a causative role in
 CC hypertension. This information can be used to find the precise role of a
 CC polymorphism in the disease, and this can be used to identify potential
 CC drugs which combat the disease. The polymorphisms can be tested for
 CC association with other diseases e.g. agammaglobulinemia, diabetes
 CC insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Miskott-Aldrich
 CC syndrome, Fabry's disease, familial hypercholesterolemia, polycystic
 CC kidney disease, hereditary spherocytosis, von Willebrand's disease,
 CC tuberous sclerosis, hereditary hemorrhagica telangiectasia, familial
 CC colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and
 CC acute intermittent porphyria. The polymorphic forms can also be used in
 CC forensics to identify individuals.
 XX
 SQ Sequence 29 BP; 4 A; 11 C; 6 G; 7 T; 1 other;

Query Match 86.7%; Score 13; DB 21; Length 29;
 Best Local Similarity 86.7%; Pred. No. 5e+03;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcggcgacgcgcgcg 15
 Db 26 GCGGAGCGACGCGCG 12
 ||||| ||||| |||||

RESULT 11
 AAF45300/c
 ID AAF45300 standard; DNA; 15 BP.
 XX
 AC AAF45300;
 XX

DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #139.
 XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU00693.
 XX
 PR 21-JUN-1999; 99US-0140345.
 XX

PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;
 XX
 DR WPI: 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by
 PT administering UV (ultra-violet) treatment (optional) and an antisense
 PT nucleic acid that inhibits or reduces growth factor mediated cell
 PT proliferation and/or inflammation -
 XX
 PS Example 6; Page 35; 201pp; English.
 CC The present invention relates to a method for ameliorating the effects
 CC of skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for insulin-like growth factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and
 CC AAF45153-F45161). The method is useful for ameliorating the effects of
 CC psoriasis, ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids,
 CC keratosis, neoplasias, scleroderma, warts, benign growths, cancers of the
 CC skin, a hyperneovascular condition such as a neovascular condition of the
 CC retina, brain or skin, growth factor mediated malignancies, other
 CC sclerotic disease, kidney disease, hyperproliferation of the inside of
 CC blood vessels or any other hyperplasia.
 XX
 SQ Sequence 15 BP; 0 A; 8 C; 5 G; 2 T; 0 other;

Query Match 82.7%; Score 12.4; DB 22; Length 15;
 Best Local Similarity 92.9%; Pred. No. 9.6e+03;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 cggcgacgcgcgcg 15
 Db 15 CAGCGGACGCGCG 2
 ||||| ||||| |||||

RESULT 12
 AAF45302/c
 ID AAF45302 standard; DNA; 15 BP.
 XX
 AC AAF45302;
 XX

DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP2 oligonucleotide #141.
 XX
 XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like growth factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU00693.
 XX
 PR 21-JUN-1999; 99US-0140345.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wraight CJ, Werther GA, Edmondson SR;

11 DNA encoding the Helicoverpa armigera granulovirus enhancer protein

The present invention relates to antisense compounds up to 30 nucleobases in length targeted to a E2F transcription factor 1. The invention is useful for inhibiting the expression of E2F transcription factor 1 in cells or tissues. The antisense oligonucleotides may also be used as a research agent and to prevent infection, inflammation or tumours.

```
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


Query Match 100.0%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 15
|||||
Db 1 GCGGCGGACGCGCG 15

RESULT 2
US-09-080-285-14
Sequence 14, Application US/09080285
Patent No. 6040181

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080, 285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
US-09-080-285-14

Query Match 100.0%; Score 15; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 15
|||||
Db 1 GCGGCGGACGCGCG 15

RESULT 3
US-08-465-485A-28
Sequence 28, Application US/08465485A
Patent No. 5831066

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 18..19
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphorothioates
US-08-465-485A-28

Query Match 86.7%; Score 13; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ggcggcgagcgagcg 13
|||||
Db 8 GCGGCGGACGCGCG 20

RESULT 4
US-09-080-285-28
Sequence 28, Application US/09080285
Patent No. 6040181

GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,285
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/465,485
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Fortney, Andrew D.
REGISTRATION NUMBER: 34,600
REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (408) 436-2070
TELEFAX: (408) 436-2075
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA
ANTI-SENSE: YES
FEATURE:
NAME/KEY: Modified_base
LOCATION: 18..19
OTHER INFORMATION: Last two internucleoside linkages are
OTHER INFORMATION: phosphothioates
US-09-080-285-28

Query Match 86.7%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 17e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggcgagcgcgc 13
|||||
DB 8 GCGGCGGCGCGC 20

RESULT 5
US-09-517-584A-13
Sequence 13, Application US/09517584A
Patent No. 6187587
GENERAL INFORMATION:
APPLICANT: Ian Popoff
APPLICANT: Vickie L. Brown-Driver

APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF E2F TRANSCRIPTION FACTOR 1 EXPRES
FILE REFERENCE: RTS-0121
CURRENT APPLICATION NUMBER: US/09/517,584A
CURRENT FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 13
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-13

Query Match 82.7%; Score 12.4; DB 4; Length 20;
Best Local Similarity 92.9%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcggcgagcgcgc 14
|||||
DB 7 gcggcgagcgcgc 20

RESULT 6
US-08-477-527A-37
Sequence 37, Application US/08477527A
Patent No. 5972599
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClellan
REGISTRATION NUMBER: 34,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

Query Match 82.7%; Score 12.4; DB 5; Length 70;
Best Local Similarity 92.9%; Pred. No. 2.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcgagcgagcgagcg 14
|||||
DB 12 GCGGCGCAGCGCG 25

RESULT 9
US-08-556-978B-53
; Sequence 53, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FAHNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; OPERATING SYSTEM: MICROSOFT WINDOWS 95
; SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556, 978B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,600
; FILING DATE: JUNE 15, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CR-9389-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-773-0164
; TELEFAX: 302-892-8112
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 75 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-556-978B-53

Query Match 82.7%; Score 12.4; DB 4; Length 75;
Best Local Similarity 92.9%; Pred. No. 2.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcgagcgagcgagcg 14
|||||
DB 45 GCGGCGCAGCGCG 58

RESULT 10
US-08-556-978B-54/C
; Sequence 54, Application US/08556978B
; Patent No. 6268169
; GENERAL INFORMATION:
; APPLICANT: FAHNESTOCK, STEPHEN F.
; TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
; TITLE OF INVENTION: SPIDER SILK ANALOGS
; FILING DATE:

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 95

SOFTWARE: MICROSOFT WORD FOR WINDOWS 95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/556, 978B

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,600

FILING DATE: JUNE 15, 1993

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: CR-9389-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-892-8112

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:

LENGTH: 75 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-556-978B-54

Query Match 82.7%; Score 12.4; DB 4; Length 75;
Best Local Similarity 92.9%; Pred. No. 2.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 gcgagcgagcgagcg 14
|||||
DB 35 GCGGCGCAGCGCG 22

RESULT 11
US-09-046-894-28
; Sequence 28, Application US/09046894
; Patent No. 6190857
; GENERAL INFORMATION:
; APPLICANT: Ralph, David
; APPLICANT: An, Gang
; APPLICANT: O'Hara, Mark S.
; TITLE OF INVENTION: DIAGNOSIS OF DISEASE STATE USING mRNA
; TITLE OF INVENTION: PROFILES IN PERIPHERAL LEUKOCYTES
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046, 894
; FILING DATE: Concurrently Herewith

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,576
FILING DATE: 24-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Nakashima, Richard A.
REGISTRATION NUMBER: P-42,023
REFERENCE/DOCKET NUMBER: UROC:014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-046-894-28

Query Match 80.0%; Score 12; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgc 12
|||||
Db 2 GCGGCGCGCAGCG 13

RESULT 12
US-09-914-961-2/c
Sequence 2, Application US/08914961
Patent No. 6018042
GENERAL INFORMATION:
APPLICANT: Mett, Helmut
APPLICANT: Haner, Robert
APPLICANT: Dean, Nicholas Mark
TITLE OF INVENTION: Antitumor Antisense Oligonucleotides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,961
FILING DATE: 20-AUG-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/287,753
FILING DATE: 09-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spivill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 4-20047/P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8615
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES

POSITION IN GENOME:
MAP POSITION: -80
UNITS: bp
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..20
OTHER INFORMATION: /note="All nucleotides are of the
phosphorothioate type"
US-08-914-961-2

Query Match 80.0%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgc 12
|||||
Db 17 GCGGCGCGCAGCG 6

RESULT 13
US-08-651-136C-43
Sequence 43, Application US/08651136C
Patent No. 6001639
GENERAL INFORMATION:
APPLICANT: Schuelein, Martin
APPLICANT: Andersen, Iene N.
APPLICANT: Lassen, Soren F.
APPLICANT: Kaupinen, Markus S.
APPLICANT: Lange, Iene
APPLICANT: Nielsen, Rudy I.
APPLICANT: Ihara, Michiko
APPLICANT: Takagi, Shinobu
TITLE OF INVENTION: No. 6001639e1 Endoglucanases
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 60016390 No. 6001639d1sk of No. 6001639th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 63 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..63
US-08-651-136C-43
Query Match 80.0%; Score 12; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 cgcgcgcgcgcgc 13
|||||
Db 9 CGCGCGCAGCCG 20

RESULT 14
; US-08-318-193-32
; Sequence 32, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; City: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid:
; DESCRIPTION: Synthetic DNA oligonucleotide
; ANTI-SENSE: YES
; US-08-318-193-32

Query Match 80.0%; Score 12; DB 1; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgc 12
|||||
Db 37 GCGCGCGCAGCG 48

RESULT 15
US-09-593-323-34
; Sequence 34, Application US/09593323
; Patent No. 6265213
; GENERAL INFORMATION:

; APPLICANT: Morgan, Antony R.
; APPLICANT: Severini, Alberto
; TITLE OF INVENTION: Compositions and Methods for Determining the Activity
; TITLE OF INVENTION: of DNA-Binding Proteins and of Initiation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: DNAB-02921
; CURRENT APPLICATION NUMBER: US/09/593,323
; CURRENT FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 09/344,300
; PRIOR FILING DATE: 1999-06-24
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-593-323-34

Query Match 78.7%; Score 11.8; DB 4; Length 18;
Best Local Similarity 86.7%; Pred. No. 5.3e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 gcgcgcgcgcgcgcgcgcgcgc 15
|||||
Db 1 gcgcgcgcgcgcgcgcgcgcgc 15

Search completed: June 28, 2002, 22:16:51
Job time: 8277 sec

Mon Jul 1 08:40:49 2002

us-09-709-170a-14.szlm75.rni

Query Match	100.0%;	Score 15;	DB 6;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 1.1e+04;		

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 15
 |||||
 Db 1 CGCGGGGCGACGGA 15

RESULT 2

A36502 69 bp DNA linear PAT 05-MAR-1997
 LOCUS Sequence 43 from Patent WO9323549.
 DEFINITION A36502
 ACCESSION A36502
 VERSION A36502.1 GI:2293813
 KEYWORDS human.
 SOURCE Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 AUTHORS Aurias,A., Delattre,O., Desmaze,C., Melot,T., Peter,M.,
 Plougastel,B., Thomas,G. and Zucman,J.
 TITLE NUCLEIC ACID CORRESPONDING TO A GENE OF CHROMOSOME 22 INVOLVED IN
 RECURRENT CHROMOSOMAL TRANSLOCATIONS ASSOCIATED WITH THE
 DEVELOPMENT OF CANCEROUS TUMORS
 JOURNAL PATENT: WO 9323549-A 43 25-NOV-1993;
 CENTRE NAT RECH SCIENC (FR)
 COMMENT Other publication FR 2691475 931126
 Other publication JP 8509647 960206.

FEATURES
 source 1..69
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 15 a 17 c 28 g 9 t
 ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 69;
 Best Local Similarity 93.3%; Pred. No. 4.1e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 15
 |||||
 Db 45 CGCGGGGCGACGGA 59

RESULT 3
 LOCUS AR080135 69 bp DNA linear PAT 31-AUG-2000
 DEFINITION Sequence 46 from patent US 5968734.
 ACCESSION AR080135
 VERSION AR080135.1 GI:10006870
 KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 69)
 AUTHORS Aurias,A., Delattre,O., Desmaze,C., Melot,T., Peter,M.,
 Plougastel,B., Thomas,G. and Zucman,J.
 TITLE Nucleic acid corresponding to a gene of chromosome 22 involved in
 recurrent chromosomal translocations associated with the
 development of cancerous tumors, and nucleic acids of fusion
 resulting from said translocations
 JOURNAL Patent: US 5968734-A 46 19-OCT-1999;
 FEATURES location/Qualifiers
 source 1..69
 /organism="unknown"
 BASE COUNT 15 a 17 c 28 g 9 t
 ORIGIN

Query Match 89.3%; Score 13.4; DB 6; Length 69;
 Best Local Similarity 93.3%; Pred. No. 4.1e+04;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 15
 |||||
 Db 45 CGCGGGGCGACGGA 59

RESULT 4

EPKRRN04 21 bp rRNA linear PLN 13-APR-1994
 LOCUS Ephedra tweediana 28S ribosomal RNA (28S rRNA), ca. bp 2019 to 2039
 DEFINITION in mature rRNA.
 ACCESSION M82019
 VERSION M82019.1 GI:471000
 KEYWORDS 28S ribosomal RNA.
 SEGMENT 4 of 5
 SOURCE Ephedra tweediana rRNA.
 ORGANISM Ephedra tweediana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Gnepophyta; Gnepopsida; Ephedrales; Ephedraceae;
 Ephedra.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Hamby,R.K., Sub.Y.B., Bult,C.J., Kallersjo,M. and Zimmer,E.A.
 TITLE Darwin's abominable mystery revisited: Ribosomal RNA insights into
 flowering plant evolution
 JOURNAL Unpublished (1991)
 REFERENCE 2 (sites)
 AUTHORS Doyle,J.A., Donoghue,M.J. and Zimmer,E.A.
 TITLE Integration of morphological and ribosomal RNA data on the origin
 of angiosperms
 JOURNAL Ann. Missouri Bot. Garden (1994) In press

FEATURES
 source 1..21
 /organism="Ephedra tweediana"
 /db_xref="taxon:3390"
 BASE COUNT 1 a 7 c 11 g 2 t
 ORIGIN

Query Match 82.7%; Score 12.4; DB 8; Length 21;
 Best Local Similarity 92.9%; Pred. No. 1.5e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 cggcgaggcgacgga 14
 |||||
 Db 8 CGCGTGGCGACGCG 21

RESULT 5
 EPKRRN04 21 bp rRNA linear PLN 15-JUN-1994
 LOCUS Ephedra distachya 28S ribosomal RNA (28S rRNA), ca. bp 2019 to 2039
 DEFINITION in mature rRNA.
 ACCESSION M82279
 VERSION M82279.1 GI:471006
 KEYWORDS 28S ribosomal RNA.
 SEGMENT 4 of 5
 SOURCE Ephedra distachya rRNA.
 ORGANISM Ephedra distachya
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Gnepophyta; Gnepopsida; Ephedrales; Ephedraceae;
 Ephedra.

REFERENCE 1 (bases 1 to 21)
 AUTHORS Hamby,R.K., Sub.Y.B., Bult,C.J., Kallersjo,M. and Zimmer,E.A.
 TITLE Darwin's abominable mystery revisited: Ribosomal RNA insights into
 flowering plant evolution
 JOURNAL Unpublished (1991)
 REFERENCE 2 (sites)
 AUTHORS Doyle,J.A., Donoghue,M.J. and Zimmer,E.A.
 TITLE Integration of morphological and ribosomal RNA data on the origin
 of angiosperms
 JOURNAL Ann. Missouri Bot. Garden (1994) In press

FEATURES
 source 1..21
 location/Qualifiers

BASE COUNT 1 a 6 c 11 g 1 t 2 others
ORIGIN

Query Match 80.0%; Score 12; DB 8; Length 21;
Best Local Similarity 85.7%; Pred. No. 2.2e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgagcgagcgagcg 14
|||||
DB 8 CGGCGGCGGCGGCG 21

RESULT 6
A48844/c A48844 18 bp DNA linear PAT 07-MAR-1997

LOCUS A48844
DEFINITION Sequence 2 from Patent EP0698787.
ACCESSION A48844
VERSION A48844.1 GI:2302506

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Rueger, P.D., Ambrosius, D.D., Schmidt, B.D., Sluka, P.D., Guder, H.D.,
Kopetzki, E., and Dr.

TITLE Electrochemical sensor
JOURNAL Patent: EP 0698787-A 2 28-FEB-1996;
BOEHRINGER MANNHEIM GMBH (DE)

COMMENT Other publication JP 8233773 960913
Other publication DE 4430023 960229.
Location/Qualifiers

FEATURES 1.18
source /organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 3 a 7 c 6 g 2 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgagcgagcgagcg 15
|||||
DB 17 CGGCGGCGGCGGCG 3

RESULT 7
AR053329/c AR053329 18 bp DNA linear PAT 29-SEP-1999

LOCUS AR053329
DEFINITION Sequence 2 from patent US 5834224.
ACCESSION AR053329
VERSION AR053329.1 GI:5978191

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 18)
AUTHORS Rueger, P., Ambrosius, D., Schmidt, B., Sluka, P., Guder, H., and
Kopetzki, E.

TITLE Electrochemical sensor containing an enzyme linked to binding
molecules bound to a noble metal surface
JOURNAL Patent: US 5834224-A 2 10-NOV-1998;
Location/Qualifiers

FEATURES 1.18
source /organism="unknown"
/db_xref="taxon:32644"

BASE COUNT 3 a 7 c 6 g 2 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgagcgagcgagcg 15
|||||
DB 20 CGGCGGCGGCGGCG 6

Query Match 78.7%; Score 11.8; DB 6; Length 18;
Best Local Similarity 86.7%; Pred. No. 2.8e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgagcgagcgagcg 15
|||||
DB 17 CGGCGGCGGCGGCG 3

RESULT 8
A78892/c A78892 24 bp DNA linear PAT 19-OCT-1999

LOCUS A78892
DEFINITION Sequence 8 from Patent EP0555894.
ACCESSION A78892
VERSION A78892.1 GI:6090463

KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 24)
AUTHORS Wool, F.R.
TITLE WHOOPING COUGH VACCINE
JOURNAL Patent: EP 0555894-A 8 18-AUG-1993;
NEDERLANDEN STAAT (NL);

FEATURES 1.24
source /organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 3 a 7 c 9 g 5 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgagcgagcgagcg 15
|||||
DB 20 CGGCGGCGGCGGCG 6

RESULT 9
AR025160/c AR025160 24 bp DNA linear PAT 05-DEC-1998

LOCUS AR025160
DEFINITION Sequence 11 from patent US 5798103.
ACCESSION AR025160
VERSION AR025160.1 GI:3977788

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)
AUTHORS Wool, F., Robert,
TITLES Whooping cough vaccine comprising a fimbria protein
JOURNAL Patent: US 5798103-A 11 25-AUG-1998;
Location/Qualifiers

FEATURES 1.24
source /organism="unknown"
/db_xref="taxon:32644"

BASE COUNT 3 a 7 c 9 g 5 t
ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 24;
Best Local Similarity 86.7%; Pred. No. 2.6e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cgagcgagcgagcg 15
|||||
DB 20 CGGCGGCGGCGGCG 6

RESULT 10
586495

LOCUS S86495 24 bp mRNA linear ROD 16-APR-2001
 DEFINITION Rattus norvegicus T cell receptor beta chain variable (TCR
 Vbeta6/Jbeta2.3) mRNA, partial cds.
 ACCESSION S86495
 VERSION S86495.1 GI:247004
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 24)
 Gold, D.P., Vainiene, M., Celtnik, B., Wiley, S., Gibbs, C., Haehlin, G.A.,
 Vandenbark, A.A. and Offner, H.
 Characterization of the immune response to a secondary
 encephalitogenic epitope of basic protein in Lewis rats. II. Biased
 T cell receptor V beta expression predominates in spinal cord
 infiltrating T cells
 J. Immunol. 148 (6), 1712-1717 (1992)
 JOURNAL 92176627
 MEDLINE 1371786
 PUBMED
 REMARK GenBank staff at the National Library of Medicine created this
 entry [NCBI gidsq 86495] from the original journal article.
 This sequence comes from Table IV.
 Location/Qualifiers
 1..24
 /organism="Rattus norvegicus"
 /strain="Lewis"
 /db_xref="taxon:10116"
 /rlnsue_type="spinal cord"
 <1..>24
 /gene="TCR Vbeta6/Jbeta2.3"
 <1..>24
 /note="TCR Vbeta6/Jbeta2.3"
 /note="This sequence comes from Table IV"
 /codon_start=1
 /product="T cell receptor beta chain variable"
 /protein_id="AAB21746.2"
 /db_xref="GI:13242921"
 /translation="IAGGARDK"
 BASE COUNT 7 a 5 c 11 g 1 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 10; Length 24;
 Best Local Similarity 86.7%; Pred. No. 2.6e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcggggagcagca 15
 ||| ||| ||| ||| ||
 Db 6 CGGGGGGGCGACAGA 20

RESULT 11
 AX116381 51 bp DNA linear PAT 11-MAY-2001
 LOCUS AX116381
 DEFINITION Sequence 1504 from Patent W00129262.
 ACCESSION AX116381
 VERSION AX116381.1 GI:14033323
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 51)
 Picoult-Newburg, L. and Pohl, M.
 Genotyping reagents, kits and methods of use thereof
 Patent: WO 0129262-A 1504 26-APR-2001;
 Orchid Biosciences, Inc. (US)
 Location/Qualifiers
 1..51
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 8 a 25 c 5 g 13 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 51;
 Best Local Similarity 86.7%; Pred. No. 2.3e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcggggagcagca 15
 ||| ||| ||| ||| ||
 Db 20 CGGGGGGGAGAGGA 6

RESULT 12
 AR159674 52 bp DNA linear PAT 17-OCT-2001
 LOCUS AR159674/C
 DEFINITION Sequence 14 from patent US 6251606.
 ACCESSION AR159674
 VERSION AR159674.1 GI:16222414
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 1 (bases 1 to 52)
 Hsue, R. and Chen, C.
 Gene sequence and method for distinguishing cordyceps sinensis
 Patent: US 6251606-A 14 26-JUN-2001;
 Location/Qualifiers
 1..52
 /organism="unknown"
 BASE COUNT 5 a 16 c 17 g 14 t
 ORIGIN

Query Match 78.7%; Score 11.8; DB 6; Length 52;
 Best Local Similarity 86.7%; Pred. No. 2.2e+05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 cggcggggagcagca 15
 ||| ||| ||| ||| ||
 Db 29 CGGGGGGGCGCGCA 15

RESULT 13
 HSTCP22B 57 bp mRNA linear PRI 18-JUL-1997
 LOCUS HSTCP22B
 DEFINITION H.sapiens mRNA for T cell receptor beta chain region
 (TCRBV21S4BJ2S3).
 ACCESSION Z49925
 VERSION Z49925.1 GI:887474
 KEYWORDS T cell receptor; T cell receptor beta chain.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 57)
 Silins, S.L.
 Direct Submision
 Submitted (23-JUN-1995) Silins S. L., Queensland Institute of
 Medical Research, EBV unit, The Pancoft Centre, 300 Herston Road,
 Brisbane, Queensland, AUSTRALIA, 4029
 2 (bases 1 to 57)
 Burrows, S.R., Silins, S.L., Moss, D.J., Khanna, R., Misko, I.S. and
 Argat, V.P.
 T cell receptor repertoire for a viral epitope in humans is
 diversified by tolerance to a background major histocompatibility
 complex antigen
 The Journal of experimental medicine. 182 (6), 1703-1715 (1995)
 JOURNAL 96096444
 MEDLINE 7500015
 PUBMED
 REFERENCE 3 (bases 1 to 57)
 Burrows, S.R., Silins, S.L., Moss, D.J., Khanna, R., Misko, I.S. and
 Argat, V.P.

TITLE T cell receptor repertoire for a viral epitope in humans is
JOURNAL J. Exp. Med. 182, 1-13 (1995)
FEATURES Location/Qualifiers
source 1..57

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PP22, PP31"
/haplotype="B8, B*4402"
/sex="Male"
/cell_type="T-lymphocyte, cytotoxic"
/tissue_type="blood"
/standard_name="T cell receptor V-D-J junctional beta chain region"
/codon_start=1
/product="TCRBV21S4BJ23 junctional region"
/protein_id="CAA90171.1"
/db_xref="GI:887475"
/translation="CASFSWTSWGATDQYFG"
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31..36
J_region 37..>38
J_segment

BASE COUNT 10 a 12 c 20 g 15 t
ORIGIN
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Best Local Similarity 86.7%; Pred. No. 2.2e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cggcgggcgacgga 15
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Db 27 CGGGGGGGCCACAGA 41

RESULT 14
LOCUS HSU91293 69 bp mRNA linear PRI 03-JUL-1997
DEFINITION Homo sapiens T-cell receptor delta chain (TCRDV3J1) mRNA, partial cds.
ACCESSION U91293.1 GI:2239991
VERSION U91293.1
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 69)
AUTHORS Holmeyer, W., Wiltfoft, T., Hennemann, A., Wlnter, H.S. and Kagnoff, M.F.
TITLE The TCR-delta repertoire in human intestine undergoes characteristic changes during fetal to adult development
JOURNAL J Immunol. 158 (12), 5632-5641 (1997)
MEDLINE 9734214
REFERENCE 2 (bases 1 to 69)
AUTHORS Holmeyer, W., Wiltfoft, T., Hennemann, A., Harland, S.W. and Kagnoff, M.F.
TITLE Direct Submission
JOURNAL Submitted (27-FEB-1997) Department of Medicine, University of Frankfurt, Theodor-Stein Kai #7, Frankfurt 60590, Germany
FEATURES Location/Qualifiers
source 1..69
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone="WS1911"
/tissue_type="colon"
/dev_stage="six weeks old"
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/gene="TCRDV3J1"

V_region
CDS

<1..>69
/gene="TCRDV3J1"
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/gene="TCRDV3J1"
/note="rearranged: contains CDR3 domain, 11 amino acids
calculation according to: Rock, E.
J. Exp. Med. 179:323-328, 1994"
/product="T-cell receptor delta chain"
/protein_id="AAC51509.1"
/db_xref="GI:2239992"
/translation="TEDSATYCAFKSVACATDKLT"
BASE COUNT 17 a 21 c 16 g 15 t
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Query Match 78.7%; Score 11.8; DB 9; Length 69;
Best Local Similarity 86.7%; Pred. No. 2.1e+05;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cggcgggcgacgga 15
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Db 45 CGCGGGGGCCACCGA 59

RESULT 15
LOCUS DUCRRN04 21 bp RNA linear PLN 13-APR-1994
DEFINITION Duchesnea indica 28S ribosomal RNA (28S RNA), ca. bp 2019 to 2039 in mature RNA.
ACCESSION M82284
VERSION M82284.1 GI:470940
KEYWORDS 28S ribosomal RNA.
SEGMENT 4 of 5
SOURCE Duchesnea indica RNA.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Duchesnea.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hamby, R.K., Suh, Y.B., Bult, C.J., Kallersjo, M. and Zimmer, E.A.
TITLE Darwin's abominable mystery revisited: Ribosomal RNA insights into flowering plant evolution
JOURNAL unpublished (1991)
REFERENCE 2 (sites)
AUTHORS Doyle, J.A., Donoghue, M.J. and Zimmer, E.A.
TITLE Integration of morphological and ribosomal RNA data on the origin of angiosperms
JOURNAL Ann. Missouri Bot. Garden (1994) In press
FEATURES Location/Qualifiers
source 1..21
/organism="Duchesnea indica"
/db_xref="taxon:13044"

BASE COUNT 1 a 6 c 10 g 1 t 3 others
ORIGIN

Query Match 76.0%; Score 11.4; DB 8; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 cggcgggcgacgga 14
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Db 8 CGCGGGGGCCACCG 21

Search completed: June 28, 2002, 22:11:17
Job time: 8368 sec

Mon Jul 1 08:40:50 2002

us-09-709-170a-15.szlm75.rge

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 28, 2002, 22:11:18 ; Search time 3762.88 Seconds
(without alignments)
100.104 Million cell updates/sec

Title: US-09-709-170a-17

Perfect score: 18
Sequence: 1 tctccagcgtgcgcacat 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 794432

Minimum DB seq length: 0
Maximum DB seq length: 75

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_on:*
21: em_or:*
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27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	18	100.0	18	6	AR052619	Sequence
2	18	100.0	18	6	AR052624	Sequence
3	18	100.0	18	6	ARI16926	Sequence
4	18	100.0	18	6	ARI40496	Sequence
5	18	100.0	18	6	ARI46347	Sequence
6	18	100.0	18	6	ARI46392	Sequence
7	18	100.0	18	6	ARI54716	Sequence
8	18	100.0	18	6	ARI67448	Sequence
9	18	100.0	18	6	AX015198	Sequence
10	18	100.0	18	6	AX020948	Sequence
11	18	100.0	18	6	AX020954	Sequence
12	18	100.0	18	6	AX040169	Sequence
13	18	100.0	18	6	AX040403	Sequence
14	18	100.0	18	6	AX063576	Sequence
15	18	100.0	18	6	AX081353	Sequence
16	18	100.0	18	6	AX083693	Sequence
17	18	100.0	18	6	AX088930	Sequence
18	18	100.0	18	6	AX103809	Sequence
19	18	100.0	18	6	AX103862	Sequence
20	18	100.0	18	6	AX103863	Sequence
21	18	100.0	18	6	AX103899	Sequence
22	18	100.0	18	6	AX105211	Sequence
23	18	100.0	18	6	AX135635	Sequence
24	18	100.0	18	6	AX283183	Sequence
25	18	100.0	18	6	AX283250	Sequence
26	18	100.0	18	6	AX355727	Sequence
27	18	100.0	18	6	AX355728	Sequence
28	18	100.0	18	6	BD009103	Sequence
29	18	100.0	18	6	196098	Sequence
30	18	100.0	18	6	AX083694	Sequence
31	18	100.0	18	6	AX083695	Sequence
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33	18	100.0	18	6	AX355729	Sequence
34	18	100.0	18	6	AX083687	Sequence
35	18	100.0	18	6	AX083688	Sequence
36	18	100.0	18	6	AR004426	Sequence
37	18	100.0	18	6	143661	Sequence
38	18	100.0	18	6	186720	Sequence
39	18	100.0	18	6	AR052604	Sequence
40	18	100.0	18	6	196083	Sequence
41	17	94.4	17	6	196090	Sequence
42	16.4	91.1	18	6	ARI46360	Sequence
43	16.4	91.1	18	6	ARI54743	Sequence
44	16.4	91.1	18	6	AX103885	Sequence
45	16.4	91.1	18	6	AX103887	Sequence

ALIGNMENTS

RESULT 1
LOCUS AR052619 18 bp DNA
DEFINITION Sequence 17 from patent US 5831066.
ACCESSION AR052619
VERSION AR052619.1 GI:5975963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 17 03-NOV-1998;
FEATURES
source location/Qualifiers
1..18
/organism="unknown"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCAGCGTGCACAT 18

RESULT 2

AR052624 18 bp DNA linear PAT 29-SEP-1999
LOCUS AR052624
DEFINITION Sequence 24 from patent US 5831066.
ACCESSION AR052624
VERSION AR052624.1 GI:5975988

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)

AUTHORS Reed,J.C.
TITLE Regulation of bcl-2 gene expression
JOURNAL Patent: US 5831066-A 24 03-NOV-1998;
FEATURES Location/Qualifiers

source 1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCAGCGTGCACAT 18

RESULT 3

AR116926 18 bp DNA linear PAT 16-MAY-2001
LOCUS AR116926
DEFINITION Sequence 1 from patent US 6140051.
ACCESSION AR116926
VERSION AR116926.1 GI:14097832

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)

AUTHORS Brown,L.R. and Xu,C.
TITLE Fluorescent dibenzazole derivatives and methods related thereto
JOURNAL Patent: US 6140051-A 1 31-OCT-2000;
FEATURES Location/Qualifiers

source 1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

ARI40496 18 bp DNA linear PAT 16-JUN-2001
LOCUS ARI40496
DEFINITION Sequence 55 from patent US 6207646.
ACCESSION ARI40496
VERSION ARI40496.1 GI:14482992

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)

AUTHORS Krieg,A.M., Kline,J., Kliman,D. and Steinberg,A.D.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6207646-A 55 27-MAR-2001;
FEATURES Location/Qualifiers

source 1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCAGCGTGCACAT 18

RESULT 5

ARI46347 18 bp DNA linear PAT 08-AUG-2001
LOCUS ARI46347
DEFINITION Sequence 59 from patent US 6218371.
ACCESSION ARI46347
VERSION ARI46347.1 GI:15109536

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)

AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
FEATURES Patent: US 6218371-A 59 17-APR-2001;
source Location/Qualifiers

source 1..18
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BASE COUNT 2 a 8 c 4 g 4 t

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCAGCGTGCACAT 18

RESULT 6

ARI46392 18 bp DNA linear PAT 08-AUG-2001
LOCUS ARI46392
DEFINITION Sequence 104 from patent US 6218371.
ACCESSION ARI46392
VERSION ARI46392.1 GI:15109581

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)

AUTHORS Krieg,A.M. and Weiner,G.
TITLE Methods and products for stimulating the immune system using
JOURNAL immunotherapeutic oligonucleotides and cytokines
FEATURES Patent: US 6218371-A 104 17-APR-2001;
source Location/Qualifiers

source 1..18
/organism="unknown"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
LOCUS AR154716 18 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 45 from patent US 6239116.
ACCESSION AR154716
VERSION AR154716.1 GI:15122769
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Krieg, A.M. and Kline, J.N.
TITLE Immunostimulatory nucleic acid molecules
JOURNAL Patent: US 6239116-A 45 29-MAY-2001;
FEATURES Location/Qualifiers
source 1..18

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
Db 1 TCTCCAGCGTGCGCCAT 18

RESULT 8
LOCUS AR167448 18 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 14 from patent US 6287591.
ACCESSION AR167448
VERSION AR167448.1 GI:17903228
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Semple, S.C., Klimuk, S.K., Harasym, T., Hope, M.J., Ansell, S.M.,
TITLE Cullis, P., Scherrer, P. and Debever, D.
JOURNAL Charged therapeutic agents encapsulated in lipid particles
PATENT: US 6287591-A 14 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..18

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
Db 1 TCTCCAGCGTGCGCCAT 18

RESULT 9
LOCUS AX015198 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 2 from Patent WO9952549.
ACCESSION AX015198
VERSION AX015198.1 GI:10041241
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 18)
AUTHORS Friede, M. and Hermand, P.
TITLE Adjuvant compositions
JOURNAL Patent: WO 9952549-A 2 21-OCT-1999;
SMITHKLINE BEECHAM BIOLOG (BE); FRIDE MARTIN (BE); HERMAND
PHILIPPE (BE)

FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/db_xref="taxon:32630"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
Db 1 TCTCCAGCGTGCGCCAT 18

RESULT 10
LOCUS AX020948 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 25 from Patent WO933868.
ACCESSION AX020948
VERSION AX020948.1 GI:10044612
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 18)
AUTHORS Dalemans, W.L. and Gerard, C.M.
TITLE Vaccine
JOURNAL Patent: WO 9933868-A 25 08-JUL-1999;
DALEMANS WILFRIED L J (BE); SMITHKLINE BEECHAM BIOLOG (BE); GERARD
CATHERINE MARIE GHISLAI (BE)
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/db_xref="taxon:32644"
/note="synthetic oligonucleotide"

BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcgcacat 18
Db 1 TCTCCAGCGTGCGCCAT 18

RESULT 11
LOCUS AX020954 18 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from Patent WO933488.

ACCESSION AX020954
VERSION AX020954.1 GI:10044617
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcccacat 18
Db 1 TCTCCAGCGTGCCTCAT 18

RESULT 12
AX040169
LOCUS AX040169 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 2 from Patent WO0062800.
ACCESSION AX040169
VERSION AX040169.1 GI:11230119
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

Query Match
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcccacat 18
Db 1 TCTCCAGCGTGCCTCAT 18

RESULT 13
AX040403
LOCUS AX040403 18 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 2 from Patent WO0062802.
ACCESSION AX040403
VERSION AX040403.1 GI:11230215
KEYWORDS
SOURCE
ORGANISM

artificial sequence.
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TCTCCAGCGTGCCTCAT 18

RESULT 14
AX063576
LOCUS AX063576 18 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 2 from Patent WO0100231.
ACCESSION AX063576
VERSION AX063576.1 GI:12541300
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
BASE COUNT
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctccagcgtgcccacat 18
Db 1 TCTCCAGCGTGCCTCAT 18

RESULT 15
AX081353
LOCUS AX081353 18 bp DNA linear PAT 27-FEB-2001
DEFINITION Sequence 32 from Patent WO0108707.
ACCESSION AX081353
VERSION AX081353.1 GI:13170195
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

FEATURES

Location/Qualifiers

source 1. 18
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
BASE COUNT 2 a 8 c 4 g 4 t
ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tctccagcgtgcgcacat 18
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Db 1 TCTCCACAGCTGCGCCAT 18

Search completed: June 28, 2002, 22:11:19
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1
2
3
4